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OM protein - protein search, using sw model

Run on: March 10, 2005, 23:36:19 ; Search time 1163 Seconds

(without alignments)
92.459 Million cell updates/sec

Title: US-09-553-431b-2

Perfect score: 1654
Sequence: 1 MASLRFFSTNHQSLLPSSL.....KAVWVEEPKRRKGFPSFGC 326

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1654	100.0	326	13	US-10-067-989-1
2	1336	80.8	326	15	US-10-424-599-217748
3	1067.5	64.5	306	16	US-10-437-963-152399
4	1047	63.3	312	16	US-10-767-701-39139
5	792	47.9	284	13	US-10-067-989-2
6	643	38.9	266	13	US-10-067-989-3
7	500.5	30.3	268	15	US-10-335-977-8662
8	479	29.0	270	13	US-10-067-989-4
9	416	25.2	174	16	US-10-767-701-58033
10	351.5	21.3	86	15	US-10-424-599-219101
11	224	13.5	294	15	US-10-335-977-9276
12	224	13.5	297	15	US-10-335-977-9277
13	209	12.6	368	15	US-10-335-977-7925

14	209	12.6	412	15	US-10-335-977-7927	Sequence 7927, Ap
15	209	12.6	425	15	US-10-335-977-7928	Sequence 7928, Ap
16	198	12.0	412	15	US-10-335-977-7926	Sequence 7926, Ap
17	197.5	11.9	279	9	US-09-738-626-6925	Sequence 6925, Ap
18	190	11.5	390	9	US-09-712-363-152	Sequence 192, App
19	179.5	10.9	294	14	US-10-032-565-7356	Sequence 7356, Ap
20	178	10.8	289	15	US-10-408-765A-1532	Sequence 1532, Ap
21	178	10.8	319	15	US-10-112-944-379	Sequence 379, App
22	176	10.6	288	9	US-09-925-298-730	Sequence 730, App
23	176	10.6	288	14	US-10-102-806-730	Sequence 730, App
24	174.5	10.6	344	15	US-10-332-288-2	Sequence 2, Appl1
25	173.5	10.5	375	9	US-09-738-626-4744	Sequence 4744, Ap
26	173.5	10.5	375	16	US-10-494-672-236	Sequence 236, App
27	173	10.5	355	15	US-10-424-599-159551	Sequence 159551, A
28	172.5	10.4	377	14	US-10-156-761-10649	Sequence 10649, A
29	171.5	10.4	338	15	US-10-282-122A-54123	Sequence 54123, A
30	171	10.3	347	15	US-10-282-122A-62873	Sequence 62873, A
31	171	10.3	347	15	US-10-282-122A-64949	Sequence 64949, A
32	170.5	10.3	426	15	US-10-424-599-170715	Sequence 170715, A
33	169	10.2	351	15	US-10-282-122A-64065	Sequence 64065, A
34	169.5	10.2	332	15	US-10-320-797-3108	Sequence 3108, Ap
35	167	10.1	287	15	US-10-282-122A-45744	Sequence 45744, A
36	164.5	9.9	478	9	US-09-738-626-3883	Sequence 3883, Ap
37	164	9.9	260	15	US-10-282-122A-44705	Sequence 44705, A
38	161.5	9.8	478	16	US-10-494-672-134	Sequence 134, App
39	160	9.7	357	14	US-10-156-761-11843	Sequence 11843, A
40	159	9.6	349	15	US-10-282-122A-61836	Sequence 61836, A
41	158.5	9.6	257	15	US-10-282-122A-65590	Sequence 65590, A
42	154.5	9.3	257	15	US-10-282-122A-65116	Sequence 65116, A
43	154.5	9.3	348	16	US-10-767-701-46969	Sequence 46969, A
44	153.5	9.3	257	15	US-10-282-122A-77571	Sequence 77571, A
45	153.5	9.3	260	15	US-10-320-797-3069	Sequence 3069, Ap

ALIGNMENTS

RESULT 1
US-10-067-989-1
; Sequence 1, Application US/10067999
; Publication No. US20020144309A1
; GENERAL INFORMATION:
; APPLICANT: Reddy, M.S. Srinivasa
; APPLICANT: Dinkins, Randy
; APPLICANT: Collins, Glenn B.
; TITLE OF INVENTION: Transgenic plants expressing Wind or Minc and an efficient
; FILE REFERENCE: 028750-219
; CURRENT APPLICATION NUMBER: US/10/067,989
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/267,488
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-067-989-1

Query Match 100.0%; Score 1654; DB 13; Length 326;
Best Local Similarity 100.0%; Pred. No. 2e-160;
Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLRFFSTNHQSLLPSSLQKTLISPRFVNNPSPRSPISVQFNKKPELAGETPRI 60
DB 1 MASLRFFSTNHQSLLPSSLQKTLISPRFVNNPSPRSPISVQFNKKPELAGETPRI 60
QY VVTSKGGVGGKTTTANNGLSLARYGFSVVAIDALGLRNLDLGLGNRVVYTCVEVI 120
DB VVTSKGGVGGKTTTANNGLSLARYGFSVVAIDALGLRNLDLGLGNRVVYTCVEVI 120
QY 121 NGDCRDLQALVNDKRWSNFELLCISKRSLPMWFGKALEVLDAKTRPEGSDFIIL 180

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Db      121 NGDCRLDQALVADKXMSNFELLCISKPSKLPMGFGGKALEMLVDALKTRPESPDITII 180
Qy      181 DCPAGIDAGFTAITPANEAVLVTPPDITLALRDADRYTGLCECGIDIMIVNRRTDM 240
Db      181 DCPAGIDAGFTAITPANEAVLVTPPDITLALRDADRYTGLCECGIDIMIVNRRTDM 240
Qy      241 IKGEDMSVLDVQEWLGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGLAEQAARL 300
Db      241 IKGEDMSVLDVQEWLGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGLAEQAARL 300
Qy      301 VEQDSMKAVWVEEPPKRGFFSFFGG 326
Db      301 VEQDSMKAVWVEEPPKRGFFSFFGG 326

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RESULT 2
US-10-424-599-217748
; Sequence 217748, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 217748
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_38653C.1.pep
US-10-424-599-217748

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Query Match      80.8%; Score 1336; DB 15; Length 326;
Best Local Similarity 80.8%; Pred. No. 7,4e-128;
Matches 269; Conservative 24; Mismatches 26; Indels 14; Gaps 6;

Qy      1 MASIRLF-----STNQSLLPSS--LSQKTLISPPFVNNRSPRSVQFNRRKPEL 53
Db      1 MPSHLLPGATYAPNSTFLRPHSPPLPSKTL--TKK--KRPKP--SALFQWNRKPEL 54
Qy      54 AGETPRIVITTSKGGVGGKTTTANGLSLARYGSVAIDADLGLRLDILLGLENNRVN 113
Db      55 SGIPTRTVITTSKGGVGGKTTTANGLSLARYGSVAIDADVGLRLDILLGLENNRVN 114
Qy      114 YTCVEVINGDCRIDQALVADKXMSNFELLCISKPSKLPMGFGGKALEMLVDALKTRPEG 173
Db      115 YTVIEVINGDCRIDQALVADKXMSNFELLCISKPSKLPMGFGGKALEMLVDALKTRPEG 174
Qy      174 SPDFIIDCPAGIDAGFTAITPANEAVLVTPPDITLALRDADRYTGLCECGIDIMIV 233
Db      175 SPDFIIDCPAGIDAGFTAITPANEAVLVTPPDITLALRDADRYTGLCECGIDIMIV 234
Qy      234 NRVRTDMIKGEDMSVLDVQEWLGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGLAE 293
Db      233 NRVRTDMIKGEDMSVLDVQEWLGLSLGVIPEDSEVIRSTNRGFPVLNKPPTLAGLAE 294
Qy      294 EQAARLVLEQDSMKAVWVEEPPKRGFFSFFGG 326
Db      295 EQAARLVLEQDSMKAVWVEEPPKRGFFSFFGG 326

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RESULT 3
US-10-437-963-152399
; Sequence 152399, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152399
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52454C.1.pep
US-10-437-963-152399

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Query Match      64.5%; Score 1067.5; DB 16; Length 306;
Best Local Similarity 68.4%; Pred. No. 2.1e-100;
Matches 216; Conservative 31; Mismatches 50; Indels 19; Gaps 5;

Qy      14 LLLPSSLSQKTLISPPFVNNRSPRSVQFNRRKPELAGETPRIVITTSKGGVGKT 73
Db      7 LLLPS-----RCPPASSPARHG-----RTAPLSGPTIRVVITTSKGGVGKT 51
Qy      74 TTTANVGLSLARYGSVAIDADLGLRLDILLGLENNRVNVCVEVINGDCRLDQALVAD 133
Db      52 TTTANVGLSLARYGSVAIDADLGLRLDILLGLENNRVNVCVEVINGDCRLDQALVAD 133
Qy      134 KRWNSFELLCISKPSKLPMGFGGKALEMLVDALKTRPESPDITIIICPAGIDAGFTA 193
Db      112 RAHDLQCLSKPSKLPGLAGSKTLTWVADALR--RAANPAFIIIDCPAGVDAFVTA 170
Qy      194 ITPANEAVLVTPPDITLALRDADRYTGLCECGIDIMIVNRRTDMIKGEDMSVLDVQ 253
Db      171 IAPAEAVLVTPPDITLALRDADRYTGLCECGIDIMIVNRRTDMIKGEDMSVLDVQ 230
Qy      254 EMGLSLGVITDESEVIRSTNRGFPVLNKPPTLAGLAEQAARLVLEQDSMKAVWVEE 313
Db      231 EMGLSLGVITDESEVIRSTNRGFPVLNKPPTLAGLAEQAARLVLEQDSMKAVWVEE 290
Qy      314 E--PKR--GFSSFFGG 326
Db      291 QERPKKAGFFSFFGG 306

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RESULT 4
US-10-767-701-39139
; Sequence 39139, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 39139
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28WAY03-C93226_1.pep
US-10-767-701-39139

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/      SOFTWARE: UNIX
/      CURRENT APPLICATION DATA:
/      APPLICATION NUMBER: US/10/335.977
/      FILING DATE: 30-DEC-2002
/      PRIOR APPLICATION DATA:
/      APPLICATION NUMBER: 08/993.002
/      FILING DATE: 17-DEC-1997
/      ATTORNEY/AGENT INFORMATION:
/      NAME: Mandragouras, Amy E.
/      REGISTRATION NUMBER: 36,207
/      REFERENCE/DOCKET NUMBER: GTN-018
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: (617)227-7400
/      TELEFAX: (617)742-4214
/      INFORMATION FOR SEQ ID NO: 8662:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 268 amino acids
/      TYPE: amino acid
/      TOPOLOGY: linear
/      MOLECULE TYPE: protein
/      HYPOTHEICAL: YES
/      ORIGINAL SOURCE:
/      ORGANISM: Helicobacter pylori
/      FEATURE:
/      NAME/KEY: misc feature
/      LOCATION: (8) LOCATION 1...268
/      SEQUENCE DESCRIPTION: SEQ ID NO: 8662:
/
US-10-335-977-8662

Query Match
Best Local Similarity 30.3%; Score 500.5; DB 15; Length 268;
Matches 109; Conservative 65; Mismatches 81; Indels 19; Gaps 5;

QY 60 IVVTSGGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERNVYTCVE 119
DB 4 VVTTSKGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERNVYTCVE 119
QY 120 INDCRDLQALVRDKRNSFELLCSKRSKLPKMGFGKALEWLVNALKTRPGSPDFI 179
DB 64 MEKCNLSQALITDKTKNSFLAASGSKOKNLDKEKVAI--LINALR---ADPDYL 117
QY 180 IDCAGIDAGFTITPANEAVLVTPPDITARDADRVGTGLECDSIR-----DIKVI 232
DB 118 IDSPAGIESGFEHALIADVALVVTPEVSLSDSRVIGIIDAKSNRAKSGEEVHKHLI 177
QY 233 VNRRTDMIKGEDMNSVLDVQEMLSLGVIPEDSEVIRSTNRGFPPLVANKPPTLAGI 292
DB 178 INRLKEVLVANGSMISIEVLKILCLPLIGIIPEDHIIISATNKGEPIV--RTDCESAKA 235
QY 293 FEQAAWRLVEQDSMKAVWVEEPKRGFPSPFGG 326
DB 236 YORITRRIIGEE---VEYVEFKAKGFPSPALKG 265

RESULT 8
US-10-067-989-4
/ Sequence 4, Application US/10067989
/ Publication No. US20020144309A1
/ GENERAL INFORMATION:
/ APPLICANT: Dinkins, Randy
/ APPLICANT: Reddy, M.S. Srinivasa
/ TITLE OF INVENTION: Transgenic plants expressing MIND or MIND and an efficient
/ FILE REFERENCE: 028750-219
/ CURRENT APPLICATION NUMBER: US/10/067.989
/ PRIOR FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: US 60/267,488
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 270

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/      TYPE: PRT
/      ORGANISM: Escherichia coli
/      US-10-067-989-4

Query Match
Best Local Similarity 29.0%; Score 479; DB 13; Length 270;
Matches 113; Conservative 58; Mismatches 82; Indels 30; Gaps 8;

QY 59 RIVVTSGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERNVYTCVE 118
DB 3 RIVVTSGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERNVYTCVE 118
QY 119 VINGCDRLQALVRDKRNSFELLCSKRSKLPKMGFGKALEWLVNALKTRPGSPDFI 178
DB 63 VINGCDRLQALVRDKRNSFELLCSKRSKLPKMGFGKALEWLVNALKTRPGSPDFI 178
QY 179 IDCPAGIDAGFTITPANEAVLVTPPDITARDADRVGTGLEC-----DGIRDIK-- 230
DB 116 VCDSPAGIETGALMALYFADRAIITTPPEVSSVRSDRIIGILASKSRRAENGEPKHEH 177
QY 231 MIVNRRTDMIKGEDMNSVLDVQEMLSLGVIPEDSEVIRSTNRGFPPLVANKPPTLAG 290
DB 178 ILITRYNPGRVSRDMLMEDVLEIRIKLVGVIPEDQSVLRASNOGEPIVLDINAD-AG 236
QY 291 LAFEQAAWRLVEQDSMKAVWVEEP-----KRGFPSPFGG 326
DB 237 KAY-----ADYERLIGEEPRFIEEKKGFLKRLFGG 270

RESULT 9
US-10-767-701-58033
/ Sequence 58033, Application US/10767701
/ Publication No. US20040172684A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21 (5353)B
/ CURRENT APPLICATION NUMBER: US/10/767.701
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 58033
/ LENGTH: 174
/ TYPE: PRT
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1) (174)
/ OTHER INFORMATION: unsure at all Xaa locations
/ OTHER INFORMATION: Clone ID: 30974845.pcp
/ US-10-767-701-58033

Query Match
Best Local Similarity 25.2%; Score 416; DB 16; Length 174;
Matches 79; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 51 PELAGTTPRIVVTSGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERN 110
DB 59 PELSGPTPRVVVVTSGKGVKTTTANVGLSLARYGFSVAIDADLGRNLDLIGLERN 118
QY 111 RVNTTCEVINGCDRLQALVRDKRNSFELLCSKRSKLPKMGFGKALEWLVNDA 166
DB 119 RVHTLTADVALAGCDRLQALVRDKRNSFELLCSKRSKLPKMGFGKALEWLVNDA 174

RESULT 10
US-10-424-599-219101
/ Sequence 219101, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:

```

```

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 265684
; SEQ ID NO 219101
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(86)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_39876C.1.pep
; US-10-424-599-219101

Query Match          21.3%; Score 351.5; DB 15; Length 86;
Best Local Similarity 82.8%; Pred. No. 6,3e-28;
Matches 72; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY      240 MKGEMMSVLVQEMLSILGVTPEDSEVIRSTNRGFLVINKPPTLAGLAFEQAAAR 299
      1 MKKREIILVLDSQKMLGPLGLGVPEDESVIRSPNRGFLVINKPPTLAGLAFEQTAWR 60
DB      300 LVEODSMKAMVVEEPEKRGFSFGG 326
      61 LVEODSMQAVVEECP-KRGFSFGG 86

RESULT 11
US-10-335-977-9276
; Sequence 9276, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7460
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...294
; SEQUENCE DESCRIPTION: SEQ ID NO: 9276:
; US-10-335-977-9276

Query Match          13.5%; Score 224; DB 15; Length 294;
Best Local Similarity 29.1%; Pred. No. 4,6e-14;
Matches 87; Conservative 40; Mismatches 106; Indels 66; Gaps 11;

QY      55 GETPRIVITSGKGVGKTTTANVGLSLARKGFSVAIDALGLRNDLLGLERNVY 114
      25 GNT-KFIATSGKGVGKSNISANLAYSLYKKGYGVFADADIGLANLDVIGVTKHN- 82
QY      115 TCVEVINGDCRDLQALVNRDKMSNFELLCISKRSLPMG-----FGKALEMLV 164
      83 -ILHALKGEAKLQ-----EITCEIFGLCLFGDSGEILKYSAGEALDRV 129
QY      165 DALKTRPEG---SPDFIIDCPAGIDAGFTTAITPANEAVLVTTPDITARDADRVGLL 221
      130 D-----EBCVLSSLDYIVDTGAGIGATQAFLNMSDCVIVITTPPSAITDA-----Y 178
QY      222 ECDGIR---DINKIVRV-----RTDMKGDMSVLVDQMLGLSLGVLP 265
      179 ACIKINSKNDLFLIANNVAQPKGRATYELFVKAKNNIAS-----LELHYLGAL 231
QY      266 EDSEVIRSTNRGFLVINKPPTLAGLAFEQAAARLVEODSMKAMVVEEPEKRGFSFG 324
      232 NSSLKRYVRKRLKLAIPNDLFSOSIDQISLVSKELTGL-----EIPKGLKSF 266

RESULT 12
US-10-335-977-9277
; Sequence 9277, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7460
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9277:

```

```

: SEQUENCE CHARACTERISTICS:
:   LENGTH: 297 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
:   HYPOTHETICAL: YES
:   ORIGINAL SOURCE:
:     ORGANISM: Helicobacter pylori
:   FEATURE:
:     NAME/KEY: misc feature
:     LOCATION: (B) LOCATION 1...297
:   SEQUENCE DESCRIPTION: SEQ ID NO: 9277:
US-10-335-977-9277

```

```

Query Match      13.5%; Score 224; DB 15; Length 297;
Best Local Similarity 29.1%; Pred. No. 4.7e-14;
Matches 87; Conservative 40; Mismatches 106; Indels 66; Gaps 11;

QY 55 GETPRIVITSGKGVGKTTTANGLSLARYGFSVAIDADLGRNLDLLGLENNVY 114
DB 28 GNT-KFAITSGKGVGKSNISANLAYSLKGYVGVFDADIGLANDVIFGVKTKN- 85
QY 115 TCVEVINGDCRLDQALVADKRNSELLCISKPSKLPWG-----FGKALEMLV 164
DB 86 -IHLHLKBAKLQ-----EICEIEPGLCLIPGDSGEILKYISGEMALDRFV 132
QY 165 DALKTRPEG---SPDFIITDCPAGIDAGFITAITPANEAVLYTTPDITALRDADRVTGLL 221
DB 133 D-----EEGVLSLDYIYIDTGAGIGATTOAFNLASDCVAVITTPDPSATLDA-----Y 181
QY 222 ECDGIR-----DIKMTVNRV-----RTDMINGEDMMSVLDVQEMLGSLGVIP 265
DB 182 ACIKNSKNKDELFLINMVAQPKRGATYERLTKVAKNNIAS-----LEHLYGAIE 234
QY 266 EDSEVIRSTNGFPLVINKPPTLAGLAFEOAMRLVQDSMKAVMVEEKRGFTSFF 324
DB 235 NSSILKRYVERKRLRIKRIAPNDLFSQSIDQIASILVSKJETGL-----EIKPKGLKSF 289

```

RESULT 13

```

US-10-335-977-7925
: Sequence 7925, Application US/10335977
: Publication No. US20040052799A1
: GENERAL INFORMATION:
:   APPLICANT: DOUGLAS SMITH et al
:   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
:     RELATING TO HELICOBACTER PYLORI FOR
:     DIAGNOSTICS AND THERAPEUTICS
:   NUMBER OF SEQUENCES: 10031
:   CORRESPONDENCE ADDRESS:
:     ADDRESSER: LAHIVE & COCKFIELD
:     STREET: 28 State Street
:     CITY: Boston
:     STATE: Massachusetts
:     COUNTRY: USA
:     ZIP: 02109-1875
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: CD-ROM ISO9660
:     COMPUTER: IBM PC Compatible
:     OPERATING SYSTEM: Windows NT 4.0
:     SOFTWARE: UNIX
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/10/335,977
:     FILING DATE: 30-Dec-2002
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: 08/993,002
:     FILING DATE: 17-DEC-1997
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Mandragouras, Amy E.
:     REGISTRATION NUMBER: 36,207
:     REFERENCE/DOCKET NUMBER: GTV-018
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (617)227-7400

```

```

: TELEFAX: (617)742-4214
: INFORMATION FOR SEQ ID NO: 7925:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 368 amino acids
:     TYPE: amino acid
:     TOPOLOGY: linear
:     MOLECULE TYPE: protein
:     HYPOTHETICAL: YES
:     ORIGINAL SOURCE:
:       ORGANISM: Helicobacter pylori
:     FEATURE:
:       NAME/KEY: misc feature
:       LOCATION: (B) LOCATION 1...368
:     SEQUENCE DESCRIPTION: SEQ ID NO: 7925:
US-10-335-977-7925

```

```

Query Match      12.6%; Score 209; DB 15; Length 368;
Best Local Similarity 24.2%; Pred. No. 2.2e-12;
Matches 80; Conservative 57; Mismatches 112; Indels 82; Gaps 12;

QY 8 STNHSLILPSLSQKTISSPRFVNPNRSPIRSVLQFNKPE-----LAGETPR 59
DB 48 SSETTSALIRENISKAMQEKGVKALNLDIKTP-----KQAPKPTTKNLAKNIKX 98
QY 60 IVVITSGKGVGKTTTANGLSLARYGFSVAIDADLGRNLDLLGLENNVYTCVEV 119
DB 99 VVMISGKGVGKSTTSVNLSALANANOKYGLDADVYGBNIPRMWGLD----- 148
QY 120 INGCRLD---QALVRDRMSNFELLCISKPSKLPWG---GKALEMLVLDLKTPE- 172
DB 149 -NADVIMDSGSKTLIPKAFG-----VSVMWSGGLLYDSGQSLIMGPMLEMAIEQ 197
QY 173 -----GSPDFIITDCPAGIDAGFIT--AITPANEAVLYTTPDITALRDAD- 216
DB 198 MLSDIIMGDLVLYVNDPPTGDAQLTLAQAVPLSAGITVTTQIYSLDARKSLDMFKX 257
QY 217 -----VTGLLE-----CDGIRDIKMTVNRVRTDMINGEDMMSVLDVQEMLGSLGVIP 266
DB 258 LHPIDAGIVENMGSFVCEHCK-----KESEIFGSMMSGLL--LEAVNQIILAKLPL 306
QY 267 DSEVIRSTNGFPLVINKPPTLAGLAFEOAA 297
DB 307 EPKVRUGDGDKEPIVISHPTSVSAKIFEKQA 337

```

RESULT 14

```

US-10-335-977-7927
: Sequence 7927, Application US/10335977
: Publication No. US20040052799A1
: GENERAL INFORMATION:
:   APPLICANT: DOUGLAS SMITH et al
:   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
:     RELATING TO HELICOBACTER PYLORI FOR
:     DIAGNOSTICS AND THERAPEUTICS
:   NUMBER OF SEQUENCES: 10031
:   CORRESPONDENCE ADDRESS:
:     ADDRESSER: LAHIVE & COCKFIELD
:     STREET: 28 State Street
:     CITY: Boston
:     STATE: Massachusetts
:     COUNTRY: USA
:     ZIP: 02109-1875
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: CD-ROM ISO9660
:     COMPUTER: IBM PC Compatible
:     OPERATING SYSTEM: Windows NT 4.0
:     SOFTWARE: UNIX
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/10/335,977
:     FILING DATE: 30-Dec-2002
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: 08/993,002
:     FILING DATE: 17-DEC-1997

```

```

/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: GTN-018
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 7927:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 412 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Helicobacter pylori
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (B) LOCATION 1...412
/ SEQUENCE DESCRIPTION: SEQ ID NO: 7927:
US-10-335-977-7927

Query Match      12.6%; Score 209; DB 15; Length 412;
Best Local Similarity 24.2%; Pred. No. 2,6e-12;
Matches 80; Conservative 57; Mismatches 112; Indels 82; Gaps 12;

QY      8 STNHGSLPLSSLSQKTLISSPRFVNPRSRPISVLOFNKRP-----LAGETPR 59
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      92 SSEETSAIRRENISKAMQKGVKALNDIKTPP-----KPOAPKPTTKNLAKNIGH 142
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 IYVITSGKGVGKTTTAVGLSLARYGFSVAIDADLGLRNLDLGLGNRVNYTCVEV 119
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      143 VMISSGKGVKSTTSVNLALANLNQKVLGDADVYGPNI PRMGIGQ----- 192
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      120 INGDCRLD---QALVDRKWSNFELLCSKPSKLPWGF---GKALEVLVDALKTRPE- 172
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      199 -NADVIMDPSGKKLIPKAFG-----VSVMGMLLYDEGQSLIRGPMLMRAIEQ 241
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      173 -----GSPDPIIIDCPAGIDAGFT--AITPANEAVLVTPDITALDADR----- 216
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      242 MLDIIMGDLVDLVVDMPPGTGDAQLTLLAQAVPLSGITVTPQIVSLDARKSLDMFKK 301
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      217 -----VTGLLE-----CDGIRDIKMI VNRVRTDMIKGEDMMSVLDVQEMIGSLIGVPE 266
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      302 LHIPIAGIYENNGSFYCEHCK-----KSEIFGNSMSGGL--LEAVNTQIILAKLPL 350
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      267 DSEVIRSTNRGFPPLVINKPPTLAGLAFEQAA 297
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      351 EPKVRIGDKGEPYIVSHPTSVSAKIFEKVA 381
      | : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-10-335-977-7928
/ Sequence 7928, Application US/10335977
/ Publication No. US20040052799A1
/ GENERAL INFORMATION:
/ APPLICANT: DOUGLAS SMITH et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
/ RELATING TO HELICOBACTER PYLORI FOR
/ DIAGNOSTICS AND THERAPEUTICS
/ NUMBER OF SEQUENCES: 10031
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 28 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: CD/ROM ISO9660
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: Windows NT 4.0
/ SOFTWARE: UNIX

```

```

/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/335,977
/ FILING DATE: 30-Dec-2002
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/993,002
/ FILING DATE: 17-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: GTN-018
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 7928:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 425 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Helicobacter pylori
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (B) LOCATION 1...425
/ SEQUENCE DESCRIPTION: SEQ ID NO: 7928:
US-10-335-977-7928

Query Match      12.6%; Score 209; DB 15; Length 425;
Best Local Similarity 24.2%; Pred. No. 2,7e-12;
Matches 80; Conservative 57; Mismatches 112; Indels 82; Gaps 12;

QY      8 STNHGSLPLSSLSQKTLISSPRFVNPRSRPISVLOFNKRP-----LAGETPR 59
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      105 SSEETSAIRRENISKAMQKGVKALNDIKTPP-----KPOAPKPTTKNLAKNIGH 155
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 IYVITSGKGVGKTTTAVGLSLARYGFSVAIDADLGLRNLDLGLGNRVNYTCVEV 119
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      156 VMISSGKGVKSTTSVNLALANLNQKVLGDADVYGPNI PRMGIGQ----- 205
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      120 INGDCRLD---QALVDRKWSNFELLCSKPSKLPWGF---GKALEVLVDALKTRPE- 172
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      206 -NADVIMDPSGKKLIPKAFG-----VSVMGMLLYDEGQSLIRGPMLMRAIEQ 254
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      173 -----GSPDPIIIDCPAGIDAGFT--AITPANEAVLVTPDITALDADR----- 216
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      255 MLDIIMGDLVDLVVDMPPGTGDAQLTLLAQAVPLSGITVTPQIVSLDARKSLDMFKK 314
      | : : : : : : : : : : : : : : : : : : : : : : : :
QY      217 -----VTGLLE-----CDGIRDIKMI VNRVRTDMIKGEDMMSVLDVQEMIGSLIGVPE 266
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      315 LHIPIAGIYENNGSFYCEHCK-----KSEIFGNSMSGGL--LEAVNTQIILAKLPL 363
      | : : : : : : : : : : : : : : : : : : : : : : : :

QY      267 DSEVIRSTNRGFPPLVINKPPTLAGLAFEQAA 297
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB      364 EPKVRIGDKGEPYIVSHPTSVSAKIFEKVA 394
      | : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: March 11, 2005, 00:16:01
Job time : 1164 secs

```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2005, 22:22:13 ; Search time 60 Seconds
(without alignments)
405.593 Million cell updates/sec

Title: US-09-553-431b-2

Perfect score: 1654

Sequence: 1 MASRLRFTNNQSLPLPSL.....KAWVEEPKRGFFSFGG 326

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	494	29.9	279	4	US-09-543-681A-4433
2	483	29.2	274	4	US-09-489-039A-14339
3	480.5	29.1	273	4	US-09-252-991A-21634
4	442	26.7	296	4	US-09-328-352-5810
5	386	23.3	181	4	US-09-540-236-3829
6	249	15.1	315	4	US-09-252-991A-27725
7	187.5	11.3	377	4	US-09-252-991A-17627
8	187.5	11.3	416	4	US-09-328-352-47660
9	179.5	10.9	364	4	US-09-248-796A-14997
10	179.5	10.9	399	4	US-09-540-236-2496
11	177.5	10.7	439	4	US-08-311-731A-118
12	168.5	10.2	381	4	US-09-489-039A-8156
13	164	9.9	267	4	US-09-328-352-7799
14	163.5	9.9	230	4	US-09-270-767-31308
15	163	9.9	299	4	US-09-270-767-41683
16	160.5	9.7	378	4	US-09-543-681A-5534
17	160	9.7	287	4	US-09-502-540-10550
18	151.5	9.2	264	4	US-09-107-532A-4581
19	147.5	8.9	226	4	US-09-583-110-3994
20	145.5	8.8	258	4	US-09-134-000C-5054
21	144	8.7	359	3	US-09-134-001C-4842
22	141	8.5	253	4	US-09-902-540-11166
23	136.5	8.3	193	4	US-09-107-433-5025
24	130.5	7.9	241	4	US-09-502-540-10075
25	130	7.9	221	4	US-09-252-991A-19158
26	130	7.9	328	4	US-09-538-092-295
27	125	7.6	255	4	US-09-198-452A-860

28	125	7.6	260	4	US-09-438-185A-807	Sequence 807, App
29	122	7.4	280	4	US-09-489-039A-11095	Sequence 11095, A
30	120.5	7.3	267	4	US-09-107-532A-5561	Sequence 5561, Ap
31	118.5	7.2	236	4	US-09-107-532A-5169	Sequence 5169, Ap
32	118	7.1	268	4	US-09-134-000C-4636	Sequence 4636, Ap
33	115.5	7.0	710	4	US-09-902-540-16023	Sequence 16023, A
34	115	7.0	264	4	US-09-540-236-3090	Sequence 3090, Ap
35	113	6.8	228	4	US-09-328-352-6189	Sequence 6189, Ap
36	108	6.5	143	4	US-09-248-796A-16948	Sequence 16948, A
37	108	6.5	259	4	US-09-634-238-246	Sequence 246, App
38	108	6.5	293	4	US-09-328-352-4836	Sequence 4836, Ap
39	107.5	6.5	308	4	US-09-050-739-94	Sequence 94, Appl
40	107.5	6.5	666	4	US-09-050-739-70	Sequence 70, Appl
41	106	6.4	312	4	US-09-252-991A-26439	Sequence 26439, A
42	102.5	6.2	116	4	US-09-621-976-4329	Sequence 4329, Ap
43	102.5	6.2	204	4	US-09-949-016-11153	Sequence 11153, A
44	101.5	6.1	285	4	US-08-311-731A-34	Sequence 34, Appl
45	101.5	6.1	285	4	US-08-311-731A-36	Sequence 36, Appl

ALIGNMENTS

```
RESULT 1
US-09-543-681A-4433
; Sequence 4433, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4433
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-4433

Query Match      29.9%; Score 494; DB 4; Length 279;
Best Local Similarity 40.8%; Pred. No. 2.9e-47;
Matches 116; Conservative 56; Mismatches 80; Indels 32; Gaps 8;

QY 59 RIVITSGKGVGKTTTANVGLSARYGSVAIDADLGLNRLDLLGLNRYNYTVE 118
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 12 RIVITSGKGVGKTTSSAISTGLAQKHKTVIDFDIGLNRLDLIMGCRRVVDVFN 71

QY 119 VINGCDRLDQALVRDRKNSFELLCTSKPRSKLPMFGSKALBWLDAKTRPESGPDIT 178
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 VINGDATTNQAIIKDKRTENLYILPASQTRDKDALTRDQ--VEQVDEL---DEMGDFDI 126

QY 179 IIDCPAGIDAGTITATPANEAVLVTPDITLRDQRTGLLEC-----DSIRDI 229
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 ICDSPGHSGLSLMALYFADDEAITTNPEVSSVRSDRLGLIAGSRPAEGEDPIKE- 185

QY 230 KAIIVRVRIDMKIGEDPMKSVLDVQEWLGLSLGLVPEDESVIRSTNRGPFVLNKPPTLA 289
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 HLLIIRYNRGVSRGMSLMEDVLELCTPLGIVIPEDOSVIRSSNQSGPVLIDSSD-A 244

QY 290 GLAFEQAMRLVEQDSMKAVVVEEP-----KRGFFS-FRGG 326
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 GRAY-----LDIVNRLGLEHFFRFRIEEKKGFLKRLRGG 279

RESULT 2
US-09-489-039A-14339
; Sequence 14339, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
```

QY 59 RIVVTSSKGVGKTTTNTAVNGSLAVYGSVAIAIDADIGLRNLDLIGLENNRVNTCYE 118
Db 7 RIIVVTSSKGVGKTTSSAAIATGLAKGKKVIIVDPIDGLRNLDIMCERRVYDDVN 66
QY 119 VINGCGRDOLVYDCKRMSNFELLCTSKPSSKILPMFGG--KALEMLVDALKTRPEGSPD 176
Db 67 VIQGDATLNQMLIKDKXTBNYLTPASQTRDKNALRRECVDVLYEEL-----KKMEFD 119
QY 177 FIIDCPAGIDAGITITATPANDVAVTTPDITLADADRVYGLEC-----DGIDIK 230
Db 120 FIVDCSANGLETGALMALYPADEAIIITTPBEVSSVRSDRILGILASSRAENGEPPIK 179
QY 231 --MIVNRFTDMIKGEDMMSVLVDCQEMLSLTLGYIPDESEVYSTIRGPFYVINKPPTL 288
Db 180 EHLLLTYYNGRNVKCDMLSMEDVETIIRINLVGVIPEDCSVLAKSNQSGEVIILDAASD- 238
QY 289 AGIAFEOAMWRLVEQDSMKAVNVVEEP-----KKRGFS--FRGG 326
Db 239 AGRAY-----ADYVERLTIGERRPRPIFEKKGGLKRLFRGG 274

```

RESULT 3
US-09-252-991A-21634
; Sequence 21634, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21634
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21634

```

[illegible]

```

Qy 173 GSPDF--111DOPAGIDAGFTTATIPNAEAVLVTTPITDRLBDRWYGLCECGIRDK 230
Db 111 LKRDYEYICDSPAGIEKGAMHLYMFADEALVTINPERSVSRBDRMLGLASKSQPAEK 170
Qy 231 -----MIVNRVITDMIKGEDMSVLDVOEMGLSLGVIPEDSEVIRSTNGFPLV 282
Db 171 GSEPIKEHLLLTRINPERVYTGKFWLGVADVEEIIATILTLGVIPESQVFLKASNGVPLV 230
Qy 283 NKRPPLAGLAFEOAAMRLVBDOSMKAVMEEPKKGFS--FEGG 326
Db 231 DEQSD-AGQAVSDAVDELTKGEIPIHRL---DVQKGFLORLFEG 271

```

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RESULT 4
US-09-328-352-5810
/ Sequence 5810, Application US/09328352
/ Patent No. 6562958
/ GENERAL INFORMATION:
/ APPLICANT: GARY L. BRETON et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
/ FILE REFERENCE: GTC99-03PA
/ CURRENT APPLICATION NUMBER: US/09/328,352
/ CURRENT FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 8252
/ SEQ ID NO 5810
/ LENGTH: 296
/ TYPE: PR1
/ ORGANISM: Acinetobacter baumannii
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (251)
/ OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk
US-09-328-352-5810

```

Query Match	26.7%;	Score 442;	DB 4;	Length 296;
Best Local Similarity	40.0%;	Pred. No. 2.5e-41;		
Matches 102;	Conservative 53;	Mismatches 84;	Indels 16;	Gaps 5;
QY	59	RIVVITSGKGVGKTTTANVGLSLARVGSVAIADIGLRNLDLLGLENRVNYTCVE	118	
Db	29	KIVVITSGKGVGKTTTASFRATGLARHKTKVVIDFDVGLRNLDTIMCERRVVYDFPN	98	
QY	119	VINGDRLQALVDPDRKMSNFELLCTISKRSKLPMGFGKALEWLVDAUKTRPEGSDDPI	178	
Db	89	VINNEKRLQALIRKDIENLYILPASQTRDQALSDGVAR--VIDELSQ---EFDDY	142	
QY	179	IIDCPAGIDAGEFITATPANEAVLVTTPDITLRADVPYGLLEC-----DGIIRDIK	230	
Db	143	ICDSFAGIERGAILAMYNADDAIIVTNPESISVRSDRIIGLGLSKTKVKEHNERIRKQ	202	
QY	231	MIVNVRDTMIGKGMMSVDV-QEMGLSLGLVPIPEDESEVIRSTRNGFPLVINKPTLA	289	
Db	203	LCITFNERADRQEMLTIIDISKDILKVPPLGVIPCECPVLQSNEXGPVILYS-ETIA	261	
QY	290	GLAFEGQAMRLVEOD 304		
Db	262	GOAVDLDLVARFLGED 276		

```

RESULT 5
US-09-540-236--3829
; Sequence 3829, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;   APPLICANT: Gary L. Breton et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
;   TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 2709.2005-001
;   CURRENT APPLICATION NUMBER: US/09/540,236
;   CURRENT FILING DATE: 2000-04-04
;   NUMBER OF SEQ ID NOS: 3840

```

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; SEQ ID NO 3829
; LENGTH: 181
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3829

```

Query Match	23.3%	Score 385	DB 4	Length 181
Best Local Similarity	48.8%	Pred. NO. 2.5e-35		
Matches 81	Conservative 36	Mismatches 41	Indels 8	Gaps 2

[illegible]

```

QY      119 VINDCDRLDQALVRKRWMSNELLCISKPRSLTPMGGG--KALEMLVDALKTRPESSPD 176
      ||:::|||||:::|:::|:::|:::|:::|:::|:::|
Db      78 VISNAKTLQALVAKDKQFENLITLPASQTRDKDALTDEGVAKVMKEILDMDKF-----D 131

```

```
QY      177 FIIDCPAGIDAGFITATIPANEAVLVTPTDITALRDADRVTGLE 222
        ||| | | : | : | : | : | : | : | : | : | : | :
db      132 FII CSPAGIERGAQLAMVHADEALIVTNPEVSSVRDSRIIGILQ 177
```

```

RESULT 6
US-09-252-991A-27725
; Sequence 27725, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIORITY FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27725
; LENGTH: 315
; TYPE: PRt
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27725

```

[illegible]

RESULT 7
US-09-252-991A-17627
; Sequence 17627, Application US/09252991A

```

: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252.991A
: PRIOR FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ. ID NOS: 33142
: SEQ. ID NO 17627
: LENGTH: 377
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
: US-09-252-991A-17627

```

Query Match	11.3%	Score 187.5	DB 4	Length 377
Best Local Similarity	25.9%	Pred. No. 2.5e-12		
Matches 70, Conservative	43	Mismatches 110	Indels 47	Gaps 9

```
QY 52 ELAGETPRIVITSGKGVKTTTANVGLSLARGFSVAIDADDLGRNDLLGLENR 111
   | : | | : | | | | | | | : | | | : : | |
Db 106 EWVGNVKNIVAVASGKGVKSTTANLALALARGARVGLDDADYVGPSCGIMFGLPEG 165
```

```

QY      112 VNTTCVEVINGDCRLDQALVRDKENMSFELLCISKSPRSKLEPMGF-----GGKALEM----- 162
           : ||::| | | : | |
Db      166 T-----RPRKREQKH--FEPL-EAHGVQVMSMAFLTDDSTPVVWRGPMVS 207

```

QY 163 --LVDAKTRPEGSPPFIILHDCPGIDAGSITAL--TPAEAVLVTPEDITLRLDADR-- 216

 DB 208 GALIQLITQTAMNDLYLVDMPEGTGDIQLTLAQKVPVAGAVITTPQDLALLDAKKGV 267

Db 268 EMFRKNIPLVLGVENMAVH---ICSNCGAHEHLPFGGGGGEKLAQ--FGVELLASHPLS 3222

```
QY      268 SEVIRKRNKGFPLVNLKRPITLGLATGQA 297
      : | | | : | : : : |
Db      323 IAIRQADSGRPVIADPESQLAMLYGEIA 352
```

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RESULT 8
US-09-328-352-4760
; Sequence 4760, Application US/09328352
; Patent No. 6562958
; APPERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4760
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4760

```

Query Match	11.3%	Score 187.5	DB 4	Length 416
Best Local Similarity	23.7%	Pred. No. 2	9e-12	
Matches 73; Conservative	51;	Mismatches	117;	Indels 67; Gaps 10

Oy 33 NNDSRSRSPIRSVLQFNRPDELACETPRIVLITSGKGVGKTTTAAVNGISLIARQFSVYA 92
 Db 137 NNP---PIQKAPQQRDVPFLHRIKAVILVSSCKGKGVKSTTTVNLALALQKMGKRGCV 192

Oy 93 IDADLIGENLDLLG-----LENRVNTCEV-----INGDCRLDQAVRDKW 136
 ::|||::|||
 ::|||::|||
 Db 193 LDDDIGRSIPMVLGNACKTPLESENVPDLAYGMVAVSIGHLTGD----- 239

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QY 137 SNFELLCISKRSPKPMGF-GKALIEWLVDALKTRPGSPDFIICCPAGIDAGFTAI- 194
Db 240 -----NNTPVAMRGPBKATGALMOLFNOGLTLPMDLVDLMIDRPETGSIQULTAQ 287
QY 195 -TPANEAVLVTTPDITALLRDADRVTLGECGIRIDIMVNRRTDM-----I 241
Db 288 RIPVGSIIITTPQNVALLDARKIELFNKVGI-PVLGVENNSTHICSNCGHEQIFGI 346
QY 242 KGEDMMSTLVDQEMGLSLGVIPEDSEVIRSTNRGFPVLANKPPTL-AGLAFEOQAWRL 300
Db 347 GGGDKLS-----EYHIFLGLRPLNQLIREHADQCKPSVIAMDADSDYIDIAKAVMOQ 401
QY 301 VEQDSMKA 308
Db 402 IERVQORA 409

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RESULT 9
US-09-248-796A-14997
; Sequence 14997, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Kelch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: 107196.132
; CURRENT FILING DATE: US/09/248,796A
; PRIOR APPLICATION NUMBER: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14997
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14997

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Query Match 10.9%; Score 179.5; DB 4; Length 364;
Best Local Similarity 24.4%; Pred. No. 1.9e-11;
Matches 73; Conservative 40; Mismatches 103; Indels 83; Gaps 11;
QY 52 ELAGETRR-----IVVITSGKGVGKTTTANVGLSLARYGFSVAIDADLGLRNIDL 104
Db 74 ELLOEVFKSIEHVKHIIILSGKGVKSSVTIQAVALLVNKGPNVGVLDIDLTPSPSLPR 133
QY 105 LLLGLENV-----NTCYEVINGDCRLDQALVRDKRMSNFELLCISKRSPKLPWGFGX 158
Db 134 MFEVENKQVHQSTRGWVPVSVNNNNNOG---TDSKRGNISLWMLG-----FLIGDRGN 184
QY 159 ALFW-----LVDAKTRPGSPDFIICCPAGIDAGFTTA-----ITPANEA 200
Db 185 SVVWRGPKKTAMIKQFLKDVWVWSAETPLDYLITTPGTSDEHIALAEELRWANPIDIKA 244
QY 201 VLVTTEDIRALDADR-----VTGLLE-----CDGIRIDIMVNRVATWIKG 243
Db 245 IIVTTPQVATADVREINFCCKVNFQILGIVENNSGFCICHGECNNITFS-----GG 298
QY 244 EDMMSVLVDQEMGLSLGVIPEDSEVIRSTNRGFPVLANKPPTLAGLAFEOQAWRLVE 302
Db 299 GKALS-----EQNLNTLYIGNVIPDPQVE-----LVLEONEKENKLLIE 337

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RESULT 10
US-09-540-236-2496
; Sequence 2496, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

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; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2496
; LENGTH: 399
; TYPE: PRT
; ORGANISM: M.cattarrhalis
US-09-540-236-2496

```

```

Query Match 10.9%; Score 179.5; DB 4; Length 399;
Best Local Similarity 25.9%; Pred. No. 2.2e-11;
Matches 74; Conservative 48; Mismatches 125; Indels 39; Gaps 11;
QY 9 TTHQSILPSSLSOKTLISSPRFVNVPERRSPIRSVLQFNKKPLAGETPRIVITSGKG 68
Db 99 TTQPNLVKTHNPTKKTDAISAQHDDKPTTXATNQ-SQLNAPHRT-----HIIAVSGKG 153
QY 69 GVGKTTTANVGLSLARYGFSVAIDADLGLRNIDLGLLENRVNVCVEVINGDCRLDQ 128
Db 154 GVGKSTTVNVALALQKMGKRVGILDADYGPSPITMLGVA-----TKRIVEN-----DQ 204
QY 129 ALVRDKRMSNFELLCISK--PRSKLPWGFG--KALEWLVDALKTRPGSPDFIICCPAG 185
Db 205 FIPIDA--NGMAVSLIGNLDAENTPIAMRGIKATGALMOLVYQTNWPOLDYLLIMPPG 262
QY 186 IDAGFTAI--TPANEAVLVTTPDITALLRDADRVTLGECGIRIDIMVNRV----- 236
Db 263 TGDQLTLAQRIPPLTGAIIYVTPQHIALDARKGVEMFHKTDIRVGLIENNALHTCTHC 322
QY 237 -RTDMI-----KGEDMMSTLVDQEMGLSLGVIPEDSEVIRSTNRG 277
Db 323 GHTEAIRFGTGGDEMAKAYDV-----PLLGQLPDDASTIRVAMDNG 362

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RESULT 11
US-08-311-731A-178
; Sequence 178, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 amino acids
; type: amino acid

```

; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mycobacterium leprae
 ; US-08-311-731A-178

Query Match 10.7%; Score 177.5; DB 4; Length 439;
 Best Local Similarity 24.3%; Pred. No. 4,3e-11;
 Matches 76; Conservative 60; Mismatches 134; Indels 43; Gaps 12;

QY 32 VNNPSRRSPDIRSVLQFN-RKPELAGETP---RIVVITSGKGVGKTTTANVGLSLARY 86
 DB 144 VMSDEQRTLRKKLRGDABEPMPFAQPNLSFRVYTVASGKGVGKSTVTMLATIAAR 203
 QY 87 GRSVAIDADLGLRNLDLGLLENRYNYCVCEVINDCDLQALVADKMSNFELLCISK 146
 DB 204 GLAVGLDADIHSHSIPRMWGSNQR-----PIQESMLPEIVHE-----VKVISIQ 251
 QY 147 -PRSKLPMGFGGKAL-----EWLVDAKTRPEGSPFIIIDCPAGID--AGFITATTPAN 198
 DB 252 FTEGNTFVWRGEMLRALQGFISDYY---WGDVLVLMIDLPRGTDIAISVAQLIPNA 307
 QY 199 EAVLVTPDITALRDADRYTGLLECDGIRDIKMIVNRVETDMIKGEDMMSVL-----DV 252
 DB 308 EILVVTTPQLAAAEVAER-AGSIALQTRQIRIVGVENMGSLMMPDGSRLQVFGEGGQGV 366
 QY 253 QEMLG-----LSLGVIPEDSEVIRSTNRGFPVLVINKPPTLAGLAFEOAMRL-VEQDS 305
 DB 367 AERLSRAVGTVPLDLPDLPALVAAGSGIPVIVNASDSPVKELRIADGLSSRQR 426
 QY 306 MKAVVVEEPKKR 318
 DB 427 LAGVSLGLDPSRR 439

RESULT 12

US-09-489-039A-8156
 ; Sequence 8156, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 8156
 ; LENGTH: 381
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 ; US-09-489-039A-8156

Query Match 10.2%; Score 168.5; DB 4; Length 381;
 Best Local Similarity 24.3%; Pred. No. 3.6e-10;
 Matches 74; Conservative 42; Mismatches 105; Indels 83; Gaps 11;

QY 41 ISSVLOFNKKPELAGTTPRIIVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGR 100
 DB 103 IATLKRVKQOPVNG-VKNITAISSGKGVGKSTVNNLALAAAGAKYGIIDADIYGP 161
 QY 101 NDLILGLR-----NRVNTCVCEVINGDCRLDQALVRDKRWSN 138
 DB 162 SIPTMGAEDSRPTSDGTHMAPIMKYGLATNSIGLVND-----DNAMV-----WR- 208
 QY 139 FELLCTSKRPSKUPMGEGKALEWLVDAKTRPEGSPDPIIIDCPAGIDAGFTAI--TP 196
 DB 209 -----GPMATKALMQMQLTLPDLDVILVLMPPGTGDIQITLLAQNP 251
 QY 197 ANEAVLVTPDITALADAR-----VTGLLECGDIRDKMIV--NRVRTMIMG 243

DB 252 VTGAVVVTPQDIALIDAKKGIWEDKEMPVLIGLE-----NMSNHICSNQHHPIFG 306
 QY 244 EDMMSVLVQEWLGLSLGIVIPEDSEVIRSTNRGFPVLVINKPPT-----LAGLAFRQ 295
 DB 307 AG-GAOKLAEKXHTQLGQWPLHITREDLDNGFTVAVRDPDSEPTDIYROLAGRNAQ 364
 QY 296 AAMR 299
 DB 365 MYWQ 368

RESULT 13

US-09-328-352-7799
 ; Sequence 7799, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 7799
 ; LENGTH: 267
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 ; US-09-328-352-7799

Query Match 9.9%; Score 164; DB 4; Length 267;
 Best Local Similarity 21.2%; Pred. No. 6.6e-10;
 Matches 62; Conservative 62; Mismatches 100; Indels 68; Gaps 10;

QY 59 RIVVITSGKGVGKTTTANVGLSLARYGFSVVAIDAD-----LGRNLDLIGLEN 110
 DB 10 QIIAIANQKGVGKTTTAVNLAASLAVLKKRVLVIDIDQGNATMGSGIQKNDLL----- 64
 QY 111 RNNYCVCEVINDCDLQALVADKMSNFELLCISKPRSKLPMGEGKALEWLVDAKLT 169
 DB 65 ---YSTVDLGEVPLETNI--OKAEVGYKVLGSNNELSGVELAIHQGREFILNALN 119
 QY 170 REGSPDPIIIDCPAGIDAGFTATTPANEAVLVTPDITALRDADRYTGLLEC-----D 224
 DB 120 EIRDSFDYIIIVCABSL-----LIT--VNLAANDGVIIIPQCEVYALE 162
 QY 225 GIRDIMIVNRVETDMIKGEDMMSVL-----DVQEWLGLSLG-VIPED 267
 DB 163 GLADLTQRTIDRIQKALNPDLFEIIGVLRTRYDARNALTRDVSALBQYFGKLVYDTVIPN 222
 QY 268 SEVIRSTNRGFPVLVINKPPTLAGLAFEOAMRLVEQDSMKAVVVEEPKKR 319
 DB 223 VRLAEPAHGLPVY-----FEKSSGAVALVNLAAEMLKSKVKKG 264

RESULT 14

US-09-270-767-33308
 ; Sequence 33308, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 33308
 ; LENGTH: 230
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-33308

Query Match
Best Local Similarity 9.9%; Score 163.5; DB 4; Length 230;
Matches 58; Conservative 29; Mismatches 83; Indels 45; Gaps 6;
QY 42 RSVLOPNRKPELAGETPRIVITSGGKVTITANVGSLARYGFSVAIDADIGLRN 101
DB 6 RNRKLLNRFIML-DVKKNVIVVLSGGGKSTVSTQSLARKNGFKVGLDIDLCPS 64
QY 102 LDLLIGLENRYNYTCVEVINGDCRLDQALVRDKRW-----SNFELLCISKPRSKLPMGF- 155
DB 65 VPYLGLEGRIFFOC-----DDGWVYVYTBESQTLAV-----MSIGPL 102
QY 156 -----GKALEMLVDALKTRPESGPDPIIDCPAGIDAGFITAITPANE----- 199
DB 103 LKNREDPVIMRGPKTMMIRQFLDVAMDELDYLIIDTPPGTSDEHITWMECLKEVGCHG 162
QY 200 AVLVTPDITALPRADRVGTGLBECGIRDKIMVN 234
DB 163 AIVVTPQEVALTDRKEITFCRKGTGINILGIVEN 197

RESULT 15
US-09-270-767-41683
; Sequence 41683, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41683
; LENGTH: 299
; TYPE: prt
; ORGANISM: Drosophila melanogaster
US-09-270-767-41683

Query Match
Best Local Similarity 9.9%; Score 163; DB 4; Length 299;
Matches 65; Conservative 34; Mismatches 95; Indels 92; Gaps 9;
QY 60 IVVITSGKGVGKTTTANVGLSLARYGFSVAIDADIGLRNLDLLGLENRVNYTCVEV 119
DB 47 IIVASGKGVGKSTVAVNFACSLAKLGRVGLDGDIFGPTIPLLMNVHG----- 97
QY 120 INGBCRLDQALVRDKRW-----SNFELLCISKPRSKLPMGF- 171
DB 98 -----EPVVDKXLMIPPOYVNVKCLSMGMLTFVETSYIMRGPLVMSAIQRLKGTD 149
QY 172 EGSPDFIINDCPAGI-DAGF-ITAITPANEAVLVTPDITALRDADRYTGLBECGIRDI 229
DB 150 WGLLDVAVIIDTPGTGDVHLSQHAPINGVILVTPHRAV-----QVT----- 194
QY 230 KMIIVNRVTDMIKGEDPMGSLVQEMTGLSLGVT----- 264
DB 195 -----LKGASM-----YEKLNVPIFGVVENMKYITCONCQRIEFPKDSRISS 237
QY 265 -----PEDESVIRSTNRGPFPLVANKPPTLACIAGIAGQAMRLVE 302
DB 238 LPRKLSLPLDSRIADSNESGVVVIKYPDSKYSGLFTQLAEITQ 283

Search completed: March 10, 2005, 23:49:14
Job time : 61 secs

QY 598 GCAATTCGTGTAACAACCTCCGATATTAACAGCGTTAAGGATGCTGATAGGGTTACGGCT 657
 Db 463 GCACTATCTCTTACCAATCCCTGAAGTTTCATCGGTACAGACTCTGATCTGATATCAATTTGT 522
 QY 658 TTGTTGAATGC 669
 Db 523 ATCTACAAAGC 534

RESULT 2

US-09-328-352-1684
 ; Sequence 1684; Application US/09328352
 ; Patent No. 6552958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GTC99-039A
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; PRIORITY FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 1684
 ; LENGTH: 891
 ; TYPE: DNA
 ; ORGANISM: Acinetobacter baumannii
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (751)
 ; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
 US-09-328-352-1684

Query Match

Best Local Similarity 8.9%; Score 87.2; DB 4; Length 891;
 Matches 258; Conservative 0; Mismatches 238; Indels 18; Gaps 1;

QY 178 ATCGTCGTATACCTCCGGAAGCGGTGTTGAAGAAGCAACACCGGAATATGTC 237
 Db 88 ATGTTGTCGTACATCAGGCAAGGCTGTAGTAACTACACAGATGATCTTTT 147
 QY 238 GGTCTCTCTCGCTCGTTAGCGTTTCTCAGTTGTCCCTTACGCCGACCTTGTCTC 297
 Db 148 GCAACAGGTTTAGCCCTTCGTGTCATAAACCTGTTGTGATGACTTTGATAGGCTTA 207
 QY 298 CGTAACTCCGATCTCCCTCAGGTTAGAGATCGATCAATTAACCTTGCCTGAGGTT 357
 Db 208 CGTAACTTGAATTAATTAATGAGGTGTGAGCGTCTGTTGTTATGATTTGCTCATGTA 267
 QY 358 ATAAAGGAGATTGCTCTCGATCAAGCTCTGTGATACGTGATACCGTTGTCGATTTTC 417
 Db 268 ATTAATATGACAGCAGCTGCAACAGCCCTTATTCGGATTAAGATATCGAAACCTT 327
 QY 418 GAATTCGTATGATATCTTAACCTGATGAAACTTCGATGGGATTTGGTGTAAAGCA 477
 Db 328 TACATTTTGGCGCTTCCCAACCCGTATAAAGATGCTTTGAGGAGCAAGGTTGCT 387
 QY 478 TTGGAATGCGTTGTGATCGTTGAAGCTTGAACCGGAAGTTCAACCGAATTCATC 537
 Db 388 CGTGAATTTGATGAGGTTTCTCAAGATTT-----GATTACATTAAT 429
 QY 538 ATCGATTGCTCGAGAAATGATGCGGATTCATAACCGCAATTAACCGGAGATGAA 597
 Db 430 TGTGATCACTCGCGGGATGACCGGTGTGCAATTTTACCAATGATACATGAGATGAA 489
 QY 598 GCAATTCGTGTAACAACCTCCGATATTAACAGCGTTAAGGATGCTGATAGGGTTACGGCT 657
 Db 490 GCAATTCGTGTAACAACCTCCGATATTAACAGCGTTAAGGATGCTGATAGGGTTACGGCT 657
 QY 658 TTGTTGAATGCATGATGATGAGATATTAAGA 691
 Db 550 ATGTTAGATGCAAAACTAAAGTTGAACACA 583

RESULT 3

US-09-543-681A-261
 ; Sequence 261; Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709,1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; PRIORITY FILING DATE: 2000-04-05
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 261
 ; LENGTH: 840
 ; TYPE: DNA
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-261

Query Match

Best Local Similarity 8.8%; Score 86.4; DB 4; Length 840;
 Matches 341; Conservative 0; Mismatches 326; Indels 39; Gaps 2;

QY 169 ACGCCGATCTCGCTGTTATCACTCCGAAAAAGCGGTGTTGAAGAAGCAACACCGC 228
 Db 28 ATGGCAGCATTTATTTGTTGTTACGTACAGTAAAGGTGGGTTGTAAACCACTTCCAGC 87
 QY 229 GCAATGTCGCTCTCTCTCGCTCGTTAAGGTTTCTCAGTTGTGCCATTTAGCCGAC 288
 Db 88 GCGGCATTTCTACCGGCTCGCTCAAAAAGGCAATAAACGGTTGTATGACTTTGAT 147
 QY 289 CTGGTCTCGTAACTCGATCTCTCTCAGGTTAGAAATCGATCAATTAACCTTGC 348
 Db 148 ATCGATTAGTATCTTAATTAATGAGGTGTGAGCGTATGAGTGTGATGACTTTGAT 207
 QY 349 GTGAGATTAAACCGAATGTCGTCTCGATCAAGCTCTGTGATGATAGCTGATAGCTT 408
 Db 208 GTTAATGATTAACAAGGATGCTACTTAATTAACAGCTTGATTAAGATTAACGATCA 267
 QY 409 TCGAATTCGATGCTATGATATCTTAACCTTATGATGAAACTTCGATGGGATTTGAT 468
 Db 268 GAAACCTTTATATCTCTCTCTCTCAACAACAGATATAA-----GAC 312
 QY 469 GGTAAAGCATGGAATGCTTGTGATGCTTGAAGAACTAGACCGGAAGTTACCGGAT 528
 Db 313 GCTTTAACCCGTATGATGATGATGAGCAAGTTGATGATGATGATGATGATGATGAT 372
 QY 529 TTGATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
 Db 373 TTTATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
 QY 589 GCGAATGAGCAGTTCTGTGTAACAACCTCCGATATTAACAGCGTTAAGGATGCTGATAGG 648
 Db 433 GCAATTAACCCATTTATCAACCAACCAAGAGTCTCTCTGTAACGATCTGAGACCGT 492
 QY 649 GTTACGGGTTTGTAG-----AATGATGATGATGATGATGATGATGATGATGATGAT 684
 Db 493 ATTTTGGATTTTATCTCTTAATCAAGCTGCGCTGAACAGCGGAATCTTATTA 552
 QY 685 ATTAAGTATTTGTGAACAGATGAACTGATATGATTAAGGAGATGATGATGATGATGAT 744
 Db 553 GAACATCTTCTATTAACAGCTATATCAAGCGGATGAAAGCGGTGATGATGATGATGAT 612
 QY 745 GTGTTAGATGTCAGAGATGTTGGATTTGATGATGATGATGATGATGATGATGATGAT 804
 Db 613 ATGGAAGATGTCATGAATTTTATGATTTCACTGCTGAGGTGTTATTCAGAGATCA 672
 QY 805 GAGTTATTCGAGACGAATGAGGTTTCCGTTGTTCTGATA 850
 Db 673 TCCGTTTACGTTATCAACCAAGGTGAGCTGTATTTCTGATA 718

RESULT 4


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US-09-489-039A-7168
; Sequence 7168, Application US/09489039A
; Patent No. 6610836
; ORGANISM: Klebsiella pneumoniae
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7168
; LENGTH: 825
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7168

Query Match
Best Local Similarity 8.7%; Score 85.2; DB 4; Length 825;
Matches 248; Conservative 0; Mismatches 213; Indels 15; Gaps 2;

QY 169 ACGCCGCGTATCGTGTATCACTCCGGAAGAGCGGTGGAAGAAGCAACACAC 228
DB 13 ATGGACGCGATTATGTGTGACTTCGGGTAAAGGGGGCGTTGGCAAGACACCTCCAGC 72

QY 229 GCAAAATGTCGTCTCTCTCTCGCTGTTCAGTTCTCAGTTGTGCCATTACGCCGAC 288
DB 73 GCGGCGCATCGCTACAGGTTGGCCCAAGAGGAGAAAGAACCGGTATTCAGCTTCGAC 132

QY 289 CTGTGCTCCGTAACCTCGATCCGCCAGGTTAGAGATCGATCAATTAACCTTGC 348
DB 133 ATCGGCTGCGTAACCTCGATTCGATTCGCTGCGAAGCGTCCGCTGTTATGATTTTC 192

QY 349 GTCGAGTTATTAACGAGATTGCTCTCGATCAAGCTCTGTAAGTGAAGCGTTGG 408
DB 133 GTCAAGCTATTCAGGCGGATCGACACAGCAAGCGGCTGATTAAGATTAAGGACAG 252

QY 409 TCGAATTTGCAATGCTATGATATCTTAACCTAGTCAAACTTCGATGGGATTTGAT 468
DB 253 GAAATCTCTACATTTCTCCGCGCTTCCAGACCGGATTAAGACGCTCTG-----ACT 306

QY 469 GGTAAAGCATTTGGAATGCTTGTGATGCGTTGAAACTAAGACCGAAGGTTACCGGAT 528
DB 307 GCGGAAGCGGTGACAAAGGTTCTCGAAGACTGAA-----GAAATGGAATTCGAT 357

QY 529 TTATCATCATGATGTTGCTCGCAGGAATCGATGCGGATTCATAACGCCATTACTCCG 588
DB 358 TTATCATGTTGTTGATTTCCCGGAGGATTTGAACCGGTCGCTGATGGCGCTTACTTT 417

QY 589 GCGAATGAAGCATTTGTTGTAACAATCCGATTAACAAGCGTTAAGGATGCTGA 644
DB 418 GCTGATGAAGCATCATCAACCACTAACCGGAAGTCTCTCGTTGCGATCCGA 473

RESULT 5
US-09-252-991A-5063
; Sequence 5063, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5063
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; LENGTH: 822
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5063

Query Match
Best Local Similarity 8.2%; Score 79.8; DB 4; Length 822;
Matches 135; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 178 ATCGTGTATCACTCCGGAAGAGCGGTGTTGAAAGACGACCAACCGCAATGTC 237
DB 16 ATCTGTAGTACTTCGGTTAAGGTTGCGTGGTTAAACCAACCAACGCGAGCTATC 75

QY 238 GGTCTCTCTCGCTCGTTACGTTTCTCAGTTTTCGCCATTGACCGGACCTGTCTC 297
DB 76 GGCACGCGCGCTGCGCTTGGCGGTTTCAAGACGTCATCGTGAAGCTTCGAGCTCGGCTG 135

QY 298 CGTAACCTCGATTCCTCTCTAGGTTAGAAATCGATCAATTAACCTTGCCTGAGTT 357
DB 136 CGTAACCTCGACCTTATCATGAGGCTGCGAACCGCGCTGTGTACGACTTCGTCAACGTC 195

QY 358 ATTAACGAGATTTGCTCTCGATCAAGCTCTGTACGATGATAGCG 404
DB 196 GTCAACGGGAGGACCACTTCAACCAAGGCTGTGATCAAGACAAAGCG 242

RESULT 6
US-09-252-991A-5154/C
; Sequence 5154, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5154
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5154

Query Match
Best Local Similarity 8.2%; Score 79.8; DB 4; Length 903;
Matches 135; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 178 ATCGTGTATCACTCCGGAAGAGCGGTGTTGAAAGACGACCAACCGCAATGTC 237
DB 876 ATCTGTAGTACTTCGGTTAAGGTTGCGTGGTTAAACCAACCAACGCGAGCTATC 817

QY 238 GGTCTCTCTCGCTCGTTACGTTTCTCAGTTTTCGCCATTGACCGGACCTGTCTC 297
DB 816 GGCACGCGCGCTGCGCTTGGCGGTTTCAAGACGTCATGTCGACTTCGACGCTGCTG 757

QY 298 CGTAACCTCGATTCCTCTCTAGGTTAGAAATCGATCAATTAACCTTGCCTGAGTT 357
DB 756 CGTAACCTCGACCTTATCATGAGGCTGCGAACCGCGGCTGTGTACGACTTCGTCAACGTC 697

QY 358 ATTAACGAGATTTGCTCTCGATCAAGCTCTGTGTAAGCTGATAGCG 404
DB 696 GTCAACGGGAGGACCACTTCAACCAAGGCTGTGATCAAGACAAAGCG 650

RESULT 7
US-09-596-002-13/C
; Sequence 13, Application US/09596002
; Patent No. 6632636
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; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Peterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 31940
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 13
; PUBLICATION INFORMATION:
; US-09-556-002-13

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Query Match
Best Local Similarity 54.2%; Score 73; DB 4; Length 31940;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

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Qy 178 ATGTGCTATATCACTCCGGAAGAGCGGTGTGGAAGACGACCAACCGCAATGTC 237
Db 273 ATGTGCTATATCACTCCGGAAGAGCGGTGTGGAAGACGACCAACCGCAATGTC 237
Qy 238 GGCTCTCTCTCGCTCGTTTACGGTTTCTCACTGTCGCAATGACCGCACTTGTGTC 297
Db 213 GGTGAGAGGCTTCTCTAGCGGTGTTAAACAGTCATCTGACTTGTGTCGTTG 154
Qy 298 CGTAACCTCGATCTCTCTAGCGGTGTTAAACAGTCATCTGACTTGTGTCGTTG 154
Db 153 CGTAATTTAGATCTAATATATGAGTTGTAATAATCGCATCTCTATGATCTTGTAGATG 94
Qy 358 ATAAACGAGATTGCGTCTGATCAAGCTCTGATCGATTAAGCGTTGTCGATTTTC 417
Db 93 ATCAGTGTATGCGCAAGCTTCTCAAGCCTTAGTCAAGACAAACAATTTGAAATCTA 34
Qy 418 GAATTTGCTATGATATCTTAAACCTAGATCGAAA 450
Db 33 TACATTTTGCCTGCATCGCAACGCGAGACAAA 1

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RESULT 8
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAYUKI
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/015
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-988-1

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Query Match
Best Local Similarity 47.1%; Score 65; DB 4; Length 640681;
Matches 249; Conservative 0; Mismatches 265; Indels 15; Gaps 1;

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Qy 167 AAAGCCCGCTATCGTCTTATACCTCCGGAAGAGCGGTGTGGAAGACGACCA 226
Db 36254 ATATGACACGGAATTAATTTAGTACTTACGAGGAAGAGGTATAGTAACTCTTAA 362465
Qy 227 CCGCAATGTCGCTCTCTCTCGCTCGTTACGGTTTCTCACTGTCGCAATTCGCG 286
Db 362464 GTGAGCTATCGGAGACGTTTACGACAAAAAGAAAAAACAATGTTATAGCTTTC 362405
Qy 287 ACCTTGCTCTCGTTAACCCTGATCTCTCTAGGTTAGAAATCGATCAATTAACCT 346
Db 362404 ATATGAGATTAAGAAATTTAGATTAATTAATGAGATGGAACGTAGACTCTATGACT 362345
Qy 347 GCGTCAGGTTATTAACGGAATGTCGTCGATCAAGCTCTGTAAGTAAAGCTT 406
Db 362344 TTATTAATGTTATTAAGATGATGACACTTAATCAAGCAATTAATTAAGATTA 362285
Qy 407 GGTGCAATTTGCAATGCTATGATATCTTAAACCTAGATCGAACTCCGATGGATTTC 466
Db 362284 CAATTAATTTGTTAATCTACCTCATCAACAACTGATTA-----G 362240
Qy 467 GTGTAAACGATTTGAATGCTTGTGATGCTTGAACCTAGACGGAAGTTCAACCG 526
Db 362239 ACGCTTTAACAAGATGAGATTGAAGTTTAAACAGAACTTATTAATAATGATTTTC 362180
Qy 527 ATTTATCATCATGATTTGCTTGCAGATCGATCCGGAATTCATTAACCGCATTAAC 586
Db 362179 ATTTATTAATTTGATTTCAACAGAGGATTAAGCGGTGCTATTTAGCAATATAT 362120
Qy 587 CGGGAATGAAGAGTTCTGTGTAACAATCCGATTAACAGCGTTAAGAGTGTGATA 646
Db 362119 TTGAGATGAAGATTAATTAATTAATTAACCCGAAATTTCTTCACTAGAGATTC 362060
Qy 647 GGGTTACGGTTTGTAGAAATGCGATGATCAGAGATTAAGATGAT 695
Db 362059 GAATTTAGAAATTAATTCATTAATCAAAAAGAGCTGAGAAAAACAT 362011

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RESULT 9
US-08-916-421b-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Built et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)

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OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (98120) .. (98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98159) .. (98159)
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc_feature
LOCATION: (98343) .. (98343)
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NAME/KEY: misc_feature
LOCATION: (231580) .. (231580)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234187) .. (234187)
OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234814) .. (234814)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (309398) .. (309398)
OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (312837) .. (312837)
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LOCATION: (855539) .. (855539)
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NAME/KEY: misc_feature
LOCATION: (1096846) .. (1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1130881) .. (1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1310988) .. (1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1313224) .. (1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349473) .. (1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349491) .. (1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1470091) .. (1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1569020) .. (1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1602912) .. (1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1603734) .. (1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1637998) .. (1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1664854) .. (1664854)
OTHER INFORMATION: n equals a, t, c, or g

US-08-916-421b-1

Query Match 5.2%; Score 50.6; DB 4; Length 1664976;
Best Local Similarity 59.3%; Pred. No. 0.00039;

Matches 86; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 182 TCGTATACCTCCGAAAGCGCGTGTGGAAAGACGACACCGCAAAATGTCGTC 241
DB 987966 TCGGATAGCATCTGGAAGAGAGTACTGGAAGCAACGATATCTGCAAACTTGTGCG 988025
QY 242 TCTCTCGCTCGTGTAGCGTTTCTCACTTGTCCCATTTGACGCCGACCTTGTCTCCGTA 301
DB 988026 TGGCTTTGGCAAAATTGGAAAAAGTGGCTGTTTGGACGCTGATATAGCAATGGCA 988085
QY 302 ACCTCGATCTCTCTCTAGGGTTAGA 326
DB 988086 ACTTAGAGCTTATCATAGGGGTTAGA 988110

RESULT 10
US-09-592-570-1

Sequence 1, Application US/09692570

Patent No. 6797466

GENERAL INFORMATION:

APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-

Patent No. 6797466

FILE REFERENCE: PB275C1

CURRENT APPLICATION NUMBER: US/09/692,570

PRIOR FILING DATE: 2003-01-14

PRIOR APPLICATION NUMBER: US 60/024,428

PRIOR FILING DATE: 1996-08-22

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1664976

TYPE: DNA

ORGANISM: Methanococcus jannaschii

FEATURE:

NAME/KEY: misc_feature

LOCATION: (28222)..(28222)

OTHER INFORMATION: n equals a, t, c, or g

FEATURE:

NAME/KEY: misc_feature

LOCATION: (28257)..(28258)

OTHER INFORMATION: n equals a, t, c, or g

FEATURE:

NAME/KEY: misc_feature

LOCATION: (84773)..(84773)

OTHER INFORMATION: n equals a, t, c, or g

FEATURE:

NAME/KEY: misc_feature

LOCATION: (84808)..(84808)

OTHER INFORMATION: n equals a, t, c, or g

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NAME/KEY: misc_feature

LOCATION: (84812)..(84812)

OTHER INFORMATION: n equals a, t, c, or g

FEATURE:

NAME/KEY: misc_feature

LOCATION: (98120)..(98120)

OTHER INFORMATION: n equals a, t, c, or g

FEATURE:

NAME/KEY: misc_feature

LOCATION: (98343)..(98343)

OTHER INFORMATION: n equals a, t, c, or g

FEATURE:

NAME/KEY: misc_feature

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OTHER INFORMATION: n equals a, t, c, or g

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FEATURE:

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OTHER INFORMATION: n equals a, t, c, or g

[illegible]

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2      COMPUTER: IBM Compatible
3      OPERATING SYSTEM: Windows
4      SOFTWARE: PaateSeq for Windows Version 2.0b
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6      APPLICATION NUMBER: US/09/221.017B
7      FILING DATE: 23-DEC-1998
8      CLASSIFICATION:
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: PP1182
11     FILING DATE: 31-DEC-1997
12     PRIOR APPLICATION DATA:
13     APPLICATION NUMBER: PP1546
14     FILING DATE: 30-JAN-1998
15     PRIOR APPLICATION DATA:
16     APPLICATION NUMBER: PP2911
17     FILING DATE: 09-APR-1998
18     PRIOR APPLICATION DATA:
19     APPLICATION NUMBER: PCT/AU98/01023
20     FILING DATE: 10-DEC-1998
21     ATTORNEY/AGENT INFORMATION:
22     NAME: Monroy, Gladys H
23     REGISTRATION NUMBER: 32,430
24     REFERENCE/DOCKET NUMBER: 27340-20021.00
25     TELECOMMUNICATION INFORMATION:
26     TELEPHONE: 650-813-5600
27     TELEFAX: 650-494-0792
28     TELEX: 706141
29     INFORMATION FOR SEQ ID NO: 1015:
30     SEQUENCE CHARACTERISTICS:
31     LENGTH: 2793 base pairs
32     TYPE: nucleic acid
33     STRANDEDNESS: double
34     TOPOLOGY: circular
35     MOLECULE TYPE: DNA (genomic)
36     HYPOTHETICAL: NO
37     ANTI-SENSE: UNKNOWN
38     ORIGINAL SOURCE:
39     ORGANISM: PORPHYROMONAS GINGIVALIS
40     FEATURE:
41     NAME/KEY: misc_feature
42     LOCATION: 1...2793
43     OS-09-221-017B-1015

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 20:49:08 ; Search time 606 Seconds
(without alignments)
9600.097 Million cell updates/sec

Title: US-09-553-431B-1

Perfect score: 978
Sequence: 1 atgcgcctctcgaatttgtt.....tctctcttcttgcgcgcg 978

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/US66_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	480.2	49.1	1419	US-10-424-599-74906	Sequence 74906, A
2	341.6	2866	18	US-10-739-930-1807	Sequence 1807, Ap
3	325.6	33.3	1183	US-10-767-701-7575	Sequence 7575, Ap
4	320	921	18	US-10-437-963-49916	Sequence 49916, A
5	237.4	24.3	2435	US-10-425-115-119462	Sequence 119462, A
6	154.2	15.8	521	US-10-021-323-6876	Sequence 6876, Ap
7	153	15.6	495269	US-10-398-221-8	Sequence 8, Appl
8	145.4	14.9	3011208	US-10-336-221-2058	Sequence 2058, Ap
9	143.8	14.7	406	US-10-424-599-76259	Sequence 76259, A
10	143.8	14.7	545	US-10-021-323-8529	Sequence 8529, Ap
11	132.4	13.5	547	US-10-767-701-26469	Sequence 26469, A

C	12	105	10.7	1987	17	US-10-398-221-3303	Sequence 3303, Ap
C	13	87.6	9.0	2731748	18	US-10-297-465A-1	Sequence 1, Appl1
C	14	81.4	8.3	807	17	US-10-335-977-3900	Sequence 3900, Ap
C	15	73	7.5	31940	17	US-10-672-787-13	Sequence 13, Appl
C	16	69.2	7.1	891	17	US-10-425-114-33547	Sequence 33547, A
C	17	68.6	7.0	499	18	US-10-425-115-15105	Sequence 15105, A
C	18	67.6	6.9	996	18	US-10-425-115-15107	Sequence 15107, A
C	19	65	6.6	640681	9	US-09-790-988-1	Sequence 1, Appl1
C	20	54.6	5.6	379	18	US-10-425-115-101244	Sequence 101244, A
C	21	46.4	4.7	2256646	18	US-10-470-565-1	Sequence 1, Appl1
C	22	42.8	4.4	885	17	US-10-335-977-4514	Sequence 4514, Ap
C	23	42.8	4.4	891	17	US-10-335-977-4515	Sequence 4515, Ap
C	24	42.4	4.3	513	17	US-10-335-977-4513	Sequence 4513, Ap
C	25	42.2	4.3	1107	17	US-10-335-977-3163	Sequence 3163, Ap
C	26	42.2	4.3	1336	17	US-10-335-977-3164	Sequence 3164, Ap
C	27	42.2	4.3	1239	17	US-10-335-977-3165	Sequence 3165, Ap
C	28	42.2	4.3	1275	17	US-10-335-977-3166	Sequence 3166, Ap
C	29	42	4.3	401	9	US-09-974-300-4671	Sequence 4671, Ap
C	30	42	4.3	2793	13	US-10-195-163-1015	Sequence 1015, Ap
C	31	40	4.1	282	17	US-10-335-977-3899	Sequence 3899, Ap
C	32	40	4.1	285	17	US-10-335-977-3898	Sequence 3898, Ap
C	33	39.8	4.1	1047	17	US-10-282-122A-25652	Sequence 25652, A
C	34	38.6	3.9	303	18	US-10-425-115-11114	Sequence 121114, A
C	35	38.2	3.9	837	9	US-09-738-626-3425	Sequence 3425, Ap
C	36	37.4	3.8	30601	10	US-09-373-658-33	Sequence 33, Appl
C	37	37.4	3.8	30601	11	US-09-989-687-33	Sequence 33, Appl
C	38	37.4	3.8	30601	11	US-09-989-687-33	Sequence 33, Appl
C	39	37	3.8	629	18	US-10-767-701-15140	Sequence 15140, A
C	40	37	3.8	768	18	US-10-767-701-15233	Sequence 15233, A
C	41	37	3.8	1038	15	US-10-156-761-6485	Sequence 6485, Ap
C	42	37	3.8	1392	18	US-10-767-701-15405	Sequence 15405, A
C	43	37	3.8	1449	17	US-10-369-493-31810	Sequence 31810, A
C	44	37	3.8	6307	17	US-10-221-714A-504	Sequence 504, App
C	45	37	3.8	6521	15	US-10-311-455-1929	Sequence 1929, Ap

ALIGNMENTS

RESULT 1
US-10-424-599-74906
; Sequence 74906, Application US/10424599
; Publication No. US20040031072A1
GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 74906
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_38653C.1
US-10-424-599-74906

Query Match 49.1%; Score 480.2; DB 17; Length 1419;
Best Local Similarity 70.2%; Pred. No. 1e-142;
Matches 644; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 58 CTTCTCAAAAGACTTAATATCTTGCACCAAGTTGCTCAATTAACCTAGCAGACGAGT 117
DB 81 CCGCCCATTCCTCCCTCTCTCCCTCCCAAAACCTTAACCCCAAAAACCCAAACCCAAA 140
QY 118 CCAATAGATCGGTTCTTCAATTATTCGCAAAACGGAATCTCGCCGAGAAACGCCGCGT 177
DB 141 CCCCCAGGCGCTGCCCCCAATGAACCGCAAGCCGAGCTCTCCGCTCCATCCGCGC 200

APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5355)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 7575
; LENGTH: 1183
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS93226_1
US-10-767-701-7575

Query Match 33.3%; Score 325.6; DB 18; Length 1183;
Best Local Similarity 64.2%; Pred. No. 3.9e-93;
Matches 506; Conservative 0; Mismatches 279; Indels 3; Gaps 1;

QY 151 CCGGAACCTCGCGGAAACCGCGGATCGCTGATACCTCCGGAAAGCGGCTGT 210
DB 121 CCGGAGCTCTCGGCGCCGACCCCGCGCTGTGTGTCTACCTCCGGAAAGCGGCTG 180
QY 211 GGAAGACGACAAACCAACCGCAATGTCGGTCTCTCTCGCTCGTTACGGTTCTCAGTT 270
DB 181 GCGAAGACCAACCACTACCGGCACTCGCGGCTCGCTCGCGGCTCGGACTCCCCGCC 240
QY 271 GTCCCATTTAGACCGGACCTGTGTCCTCGTAACTTCGATCTCTCTCTGAGTTAGAGANT 330
DB 241 GTCCCGGTGACGCGGACCGCGGCTCGCAACTCGACCTCTGCTCGGCTCGGAAAC 300
QY 331 CGAGTCATTAACATCTTGCTCGAGGTATTAACGAGATTGTCTGTCTGATCAAGTCTG 390
DB 301 CGCGTCACCTACCGCGCGCGACGCTCGCTGGGAGCTGAGGCTGCACGAGCGCTC 360
QY 391 GACAGGATTAACGCTGTGTGCAATTTGCAATGCTATGATATCTAAACCTAGATCGAAA 450
DB 361 GTCCGACACCGCGCGCTCCAGAGACTCTCACTCTCTGCTCTCCAGGCAAGCTTCAG 420
QY 451 CTTCCGATGGATTGTGTGTAAAGCATTTGGAATGGCTTGTGAGTCGTTGAAACTAGA 510
DB 421 CTGCGCTCGGCTTGGGATCGAAGACCTCACCTGGGTGCGCGAGCGCT--TCGGCGC 477
QY 511 CCGGAAGCTTACCGGATTTCTCATCATCATGATTTGTCCTCGAGGAATCATGCGGATTC 570
DB 478 TCGCCTAACACCGCGCTTCTCATCTCATGACTGCTCCGCGAGGTGTGATCCGGGTT 537
QY 571 ATACCGCATTAACCTCGGCGAATGAAGGATTTCTGTAACAACCTCGGATTTAAACGCG 630
DB 538 GTCACTGCCATTGACCTCGAGAGAGGAGAGGAGTGTGTAACACCTTACATTCAGGCT 597
QY 631 TTAAGGATGCTGATAGGGTTACGGGTTTGTAGATGCGATGGAATCAGAGATATTAAG 690
DB 598 CTCGCGATGCTGACCGGTGTCCAGAGACTGTGAGATGCGATGCGATCAAGATATCAAG 657
QY 691 ATGATTGTGAACAGAGTGAAGTGTATGATTTAAAGGAGAGATATGATGTCAGTTA 750
DB 658 ATTATTGTCAACCGAGTGTGCGCAGACTGTGTAAGGGGAGAGACATGATGTCAAGGCTT 717
QY 751 GATGTCAGAGAGATGTTGGGATTTGTCATTTGTTGTTGTAATTAAGCTTCTTGAAGTT 810
DB 718 GATGTCAGAGAGATGTTGGGATTTGTCATTTGTTGTTGTTGTTGTTGTTGTTGTTG 777
QY 811 ATTGAGACGAGATGAGAGGTTTCCGCTTGTCTGTAATTAAGCTTCTTGAAGTTGCGGA 870
DB 778 ATCCGAGATCAAAATAGGGGTGTGCCATTGGTGTCAACGACCGCGCAAGCTGCGGC 837
QY 871 TTGGGCTTTGAGACGCGGCTTGAGAGCTGCTTGAAGATATGATGTAAGCTGTTAG 930
DB 838 CTTCGCTGTGACGAGCGCACTGGCGATTGTGGAAGAGATGCGATGACAGCATGATG 897
QY 931 GTGAGGA 938
| | | | |

DB 898 GTGAGGA 905

RESULT 4
US-10-437-963-49916
; Sequence 49916, Application US/10437963
; Publication No. US20040123343A1

GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49916
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52454C.1
US-10-437-963-49916

Query Match 32.7%; Score 320; DB 18; Length 921;
Best Local Similarity 63.3%; Pred. No. 2.1e-91;
Matches 529; Conservative 0; Mismatches 295; Indels 12; Gaps 2;

QY 151 CCGGAACCTCGCGGAAACCGCGGATCGCTGATACCTCCGGAAAGCGGCTGT 210
DB 85 CCGGAGCTCTCGGCGCCGACCCCGCGCTGTGTGTCTACCTCCGGAAAGCGGCTG 144
QY 211 GGAAGACGACAAACCAACCGCAATGTCGGTCTCTCTCGCTCGTTACGGTTCTCAGTT 270
DB 145 GGTAAAGACCAACCAACCGGCAATCTCGCGGCTCTCTCGAGGCTCTCTCGGCT 204
QY 271 GTCCCATTTAGACCGGACCTGTGTCCTCGTAACTTCGATCTCTCTGAGTTAGAGANT 330
DB 205 GTCCGCTGACGCGGACCGGCTCGGCAATCTGAGACTCTCTCGGCTCGAGAAC 264
QY 331 CGAGTCATTAACATCTTGCTCGAGGTATTAACGAGATTGTCTGTGATCAAGCTCTG 390
DB 265 CGCGTCACCTACCGCGCGCGACGTCGCTGGGAGACTGCGGCTCGACGAGGCTC 324
QY 391 GACGATTAACCGTTGTCGAATTTGCAATGCTATGATATCTAAACCTAGATCGAAA 450
DB 325 GTCCGACACCGCGCGCTCCATGACCTGAGCTGCTGCTCCAGGCGCGCTCAAG 384
QY 451 CTTCCGATGGATTGTGTGTAAAGCATTTGGAATGGCTTGTGAGTCGTTGAAACTAGA 510
DB 385 CTGCGCTCGCTTGGCTTCAAGACCTCACTGAGTGTGTCAGCGCT--TCGCC 441
QY 511 CCGGAAGCTTACCGGATTTCTCATCATCATGATTTGTCCTCGAGGAATCATGCGGATTC 570
DB 442 GCGGCAACCGACCGGCTTCTCATCTCATGACTGCTCGAGGTGTGATGAGAGGTT 501
QY 571 ATACCGCATTAACCTCGGCGAATGAAGGATTTGTTAACTCCGATATTAACGCG 630
DB 502 GTCACTGCTATTCCTCGCAGAGGCGGCTGTGTGATCAACCTTACATTCAGGCT 561
QY 631 TTAAGGATGCTGATAGGGTTACGGGTTTGTAGATGCGATGGAATCAGAGATATTAAG 690
DB 562 CTCGCGATGCTGACCGGTGTGAGGCTTATGAGTGTGAGGCTATCAAGATTAAG 621
QY 691 ATGATTGTGAACAGAGTGAAGCTGATATGATTTAAAGGAGAGATATGATGTCAGTTA 750
DB 622 ATTATTGTCAACGAGTACCGCAGACTGTGTAAGGAGAGATATGATGTCAAGCTT 681
| | | | |

Qy 751 GATGTGACGAGATGTTGGATTGCTATTCCTGTGATATTCCTGAAGATTCGAGTT 810
 Db 682 GATTTTAAAGAAAAGCTTGCTTCTTCTGATGTTGTGTGACAGAGACCGGAGGTG 741
 Qy 811 ATTCGAAGACGAATCGAGGTTTCGCTTGTCTGAATTAAGCTTCTTAAGCTTCGAG 870
 Db 742 ATCCGAGTACAAATAGAGTGTGCGGTGTCTGAACGACCCACACACAGCTGCT 801
 Qy 871 TTGGCGTTTGAAGCGGCGCTTGGAGACTGTGACAAATAGATGAAGGCTGTATG 930
 Db 802 CTTCCTCTGAGAGCGGAGCTTGGCGGTGTGGAAGAGATGCAATGACAGCACTTATG 861
 Qy 931 GTGAGGAGA-----ACCTAAGAACGTGCTTCTTCTTTCTTTGGCGG 977
 Db 862 GTAGAGGAGCAGAGAGGCGCCCAAGAAAGAGCTGGGTTCTTCTTCTTTGGTGG 917

RESULT 5
 US-10-425-115-119462/c
 ; Sequence 119462, Application US/10425115
 ; Publication No. US2004021422A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53222) B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 119462
 ; LENGTH: 2435
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MFT4577_40432C.1
 US-10-425-115-119462

Query Match 24.3%; Score 237.4; DB 18; Length 2435;
 Best Local Similarity 63.8%; Pred. No. 1.2e-64;
 Matches 377; Conservative 0; Mismatches 211; Indels 3; Gaps 1;
 Qy 348 CGTCGAGGTTATTAACGAGATTTGCTCTCGATCAAGCTTGTGATGAAGCTTGG 407
 Db 2399 CGCCGAGCTCTCGCGGAGACTGCGACTGACACGAGGCGTCTGCCACCGCGGCT 2340
 Qy 408 GTGGAATTTGGAATTCATATGTAATCTAACTAGATCGAAACTTCGAGTGGATTGG 467
 Db 2339 CCAGGACCTCCACCTCTGCTCTCCAGCCCGCTCCAGCTGCCCCCTCGGTTGG 2280
 Qy 468 TGTGAAGCATTTGAATGGCTTGTGATGCGCTTGAACCTAGACCGGAAGTTACCGGA 527
 Db 2279 ATCCAAAGACCTCACCTGAGTGTGCGAGCGCTACGAC---GCTCGACAGCCACCGC 2223
 Qy 528 TTTTCATCATCATCATGTTGCTCTGCAAGATGATGCGGATTCATTAACCGCATTAATCC 587
 Db 2222 ATTCAATCCATCATGACTGCCCCGAGGTGTGATGCTGGGTTTCTACTGCAATGGACC 2163
 Qy 588 GCGGATGAAGCAGTTCTGTGTAACAATCCGAGATTAACAGCGTTAAGGATGCTGATAG 647
 Db 2162 CGCAAAAGAGCGGCTGCTGTTACCATCCCGAATTAACGCTCTCCGAGATGCTGACCG 2103
 Qy 648 GCTTAAGGCTTTTGTAGATCGATGATGATGATGATGATGATGATGATGATGATGATG 707
 Db 2102 TGTGCGCGGAGCTGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2043
 Qy 708 GAGAAGTATATGATTAAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 767
 Db 2042 GCGGCGAGACTGCTGTGAAGGAGGAGCATGATGATGATGATGATGATGATGATGATGATG 1983

Qy 768 GGGATGTCTATTCCTGTTGTTATTCCTGAAGATTTCTGAGTTATTGGAAGACGAATCG 827
 Db 1982 CGGGTGTGCTTTACTAGAGGCTGTGTGCGAGAGACAGGAGGTGATCCGAGATGACGAATAG 1923
 Qy 828 AGGTTTCCGCTTGTCTTGAATTAAGCTTCTACGCTTCGAGGATGAGGCTTTGAGAGGC 887
 Db 1922 GGGCGGCGCGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1863
 Qy 888 GGGTTGAGACTCGTTGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 938
 Db 1862 TACTTGAGATTTGTGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 1812

RESULT 6
 US-10-021-323-6876/c
 ; Sequence 6876, Application US/10021323
 ; Publication No. US20040123340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Deikman, Jill
 ; APPLICANT: Feng, Paul C.C.
 ; APPLICANT: Fincher, Karen L.
 ; APPLICANT: Ziegler, Todd E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(52274) B
 ; CURRENT APPLICATION NUMBER: US/10/021,323
 ; CURRENT FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: US 60/255, 619
 ; PRIOR FILING DATE: 2000-12-14
 ; NUMBER OF SEQ ID NOS: 17880
 ; SEQ ID NO 6876
 ; LENGTH: 521
 ; TYPE: DNA
 ; ORGANISM: Goseypium hirsutum
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3828-011-Q1-N6-D10
 US-10-021-323-6876

Query Match 15.8%; Score 154.2; DB 18; Length 521;
 Best Local Similarity 82.3%; Pred. No. 2.5e-38;
 Matches 177; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 Qy 764 TGTGGATTTGTCATTCCTGTTGTTATTCCTGAAGATTCGAGTTATTGGAAGACGA 823
 Db 521 TGTGTGGATTTGTCATTCCTGTTGTTATTCCTGAAGATTCGAGTTATTGGAAGACGA 462
 Qy 824 ATCGAGGCTTTCGCTGTTCTGAATAAGCTCTGAGCTTGGCGGATTTGGCTTTGAGC 883
 Db 461 ACAGAGGGTACCACTTGTCTGAATAAGCTCTGAGCTTGGCGGATTTGGCTTTGAGC 402
 Qy 884 AGCGGCTTGAAGACTGCTTGAAGCAAGATGATGAAAGGCTTTATGTTGAGGAGAAAC 943
 Db 401 AAGCGCTTGAAGGCTGTTGAGCAAGATGATGAAAGGCTTTATGTTGAGGAGAGC 342
 Qy 944 CTAGAAACGTGCTTCTTCTTTCTTTGGCGGC 978
 Db 341 CCAAAAGCGTGGGTTTCTCATTTTGTGAGGC 307

RESULT 7
 US-10-398-221-8
 ; Sequence 8, Application US/10398221
 ; Publication No. US2004018514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNST, Frederick
 ; APPLICANT: GLASER, Philippe
 ; TITLE OF INVENTION: Listeria innocua, genome and applications
 ; FILE REFERENCE: 344 702 - US
 ; CURRENT APPLICATION NUMBER: US/10/398,221
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 ; PRIOR FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: FR 00/12 697

```
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: Patencin version 3.0
/ SEQ ID NO: 8
/ LENGTH: 495269
/ TYPE: DNA
/ ORGANISM: Listeria innocua
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(end)
/ OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-8
```

```
Query Match      15.6%; Score 153; DB 17; Length 495269;
Best Local Similarity 53.4%; Pred. No. 3.9e-36;
Matches 355; Conservative 0; Mismatches 295; Indels 15; Gaps 1;
```

```
QY 182 TCGTTATACCTCCGGAAAGCGGTGTGGAAGAAGACGACAAACACCGGAAATGTCGTC 241
DB 175073 TAGTCATTACTTCTGGGAAAGGTGAGTAGGAAAACTTCACTGCTAACTTAGAA 175132
QY 242 TCTCTCTCGCTGTTACGGTTTCTCAGTTGTGCCATTACGCCGACCTTGGTCTCCGTA 301
DB 175133 CGGCACTTCTCTTCAAGGTAAAGAGTGTGCTTGTATGATATGATATCGGCTTCGTA 175192
QY 302 ACCCGATCTCCTCCTAGGGTTAGAGATCGAGTCATTAACCTTGCAGGTTATTA 361
DB 175193 ATTATGATGTGTCTAGAGCCTTGAAGATCGATTTATATGATTTAGATGTTGTG 175252
QY 362 ACGGAGATGTGCTCTCGATCAAGCTCTGTATCGTATAGGCTTGGTGCATTTGCAAT 421
DB 175253 AAGGACGCTGCAAAATCCATCAAGCTATGATTAAGATTAAGGTTTGTATGATTTACTT 175312
QY 422 TGCATATGATATCTAAACCTAGATGAAACTTCCGATGGGATTTGGTGAAGCATTTGG 481
DB 175313 TCTTACTTCCAGCAGACAAACTACGGA-----TAAAAATGCTGTTCCG 175357
QY 482 AATGCTGTGATGCGTTGAAAACTAGACCGGAAGTTACCGGATTTTCATCATCATG 541
DB 175358 GGAACAAATGATAGAGCTAATTAATCACTACGTCCTGATTAACGATTAATTTCTAATG 175417
QY 542 ATTGTCCTGCAAGAAATCGATGCGGATTCATTAACCGCATTTACTCCGGGAAATGAAGCAG 601
DB 175418 ATTGCCACGACGAAGATTTGAACAGATATTAATAATCGGTTGCTGAGCTGATTAAGCAA 175477
QY 602 TTCTGTGTAACAATCCGATATTAACAGCGTTAAGGATGCTGATAGGGTTACGGTTGT 661
DB 175478 TTGTTGTGACTACTCCAGAGATTTTCAGCTGTTGAGATGCGGACAGAAATTAATGCGTTGC 175537
QY 662 TAGAATGCGATGGAATCAGAGATATTAAGATGATTTGTGAACAGAGTGAACATGATATGA 721
DB 175538 TTGAAAAAAGAGATATTTGAGCCACCAAACTTATTAATCAATGATATTCATCAACAATGA 175597
QY 722 TTAAGAGAGAGATATGATGTCAGTGTATGATGTGACAGAGATGTTGGAGTTGTCATTCG 781
DB 175598 TGGTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 175657
QY 782 TTGGTGTAAATTCCTGAAGATTTCTGAGTTATTCGAAGCAAGATCGAGGATTTCCGCTTG 841
DB 175658 TTGGTGTAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 175717
QY 842 TTCTG 846
DB 175718 CGATG 175722
```

```
RESULT 8
US-10-398-221-2058/c
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
```

```
/ TITLE OF INVENTION: Listeria innocua, genome and applications
/ FILE REFERENCE: 344 702 - US
/ CURRENT APPLICATION NUMBER: US/10/398,221
/ CURRENT FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: FR 00/12 697
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 4025
/ SOFTWARE: Patencin version 3.0
/ SEQ ID NO: 2058
/ LENGTH: 3011208
/ TYPE: DNA
/ ORGANISM: Listeria innocua
US-10-398-221-2058
```

```
Query Match      15.6%; Score 153; DB 17; Length 3011208;
Best Local Similarity 53.4%; Pred. No. 1.2e-35;
Matches 355; Conservative 0; Mismatches 295; Indels 15; Gaps 1;
```

```
QY 182 TCGTTATACCTCCGGAAAGCGGTGTGGAAGAAGACGACAAACACCGGAAATGTCGTC 241
DB 1583882 TAGTCATTACTTCTGGGAAAGGTGAGTAGGAAAACTTCACTGCTAACTTAGAA 1583823
QY 242 TCTCTCTCGCTGTTACGGTTTCTCAGTTGTGCCATTAGACGCCGACCTTGGTCTCCGTA 301
DB 1583822 CGGCACTTCTCTTCAAGGTAAAGAGTGTGCTTATGATATGATATCGGCTTCGTA 1583763
QY 302 ACCCGATCTCCTCCTAGGGTTAGAGATCGAGTCATTAACCTTGCAGTGCAGTTATTA 361
DB 1583762 ATTATGATGTGTCTAGAGCCTTGAAGATCGATTTATATGATTTAGATGATGTTGTG 1583703
QY 362 ACGGAGATGTGCTCTCGATCAAGCTCTGTATCGTATAGGCTTGGTGCATTTGCAAT 421
DB 1583702 AAGGACGCTGCAAAATCCATCAAGCTATGATTAAGATTAAGGTTTGTATGATTTACTT 1583643
QY 422 TGCATATGATATCTAAACCTAGATGAAACTTCCGATGGGATTTGGTGAAGCATTTGG 481
DB 1583642 TCTTACTTCCAGCAGACAAACTACGGA-----TAAAAATGCTGTTCCG 1583598
QY 482 AATGCTGTGATGCGTTGAAAACTAGACCGGAAGTTACCGGATTTTCATCATCATG 541
DB 1583597 GGAACAAATGATAGAGCTAATTAATCACTACGTCCTGATTAACGATTAATTTCTAATG 1583538
QY 542 ATTGTCCTGCAAGAAATCGATGCGGATTCATTAACCGCATTTACTCCGGGAAATGAAGCAG 601
DB 1583537 ATTGCCACGACGAAGATTTGAACAGATATTAATAATCGGTTGCTGAGCTGATTAAGCAA 1583478
QY 602 TTCTGTGTAACAATCCGATATTAACAGCGTTAAGGATGCTGATAGGGTTACCGGTTTGT 661
DB 1583477 TTGTTGTGACTACTCCAGAGATTTTCAGCTGTTGAGATGCGGACAGAAATTAATGCGTTGC 1583418
QY 662 TAGAATGCGATGGAATCAGAGATATTAAGATGATTTGTGAACAGAGTGAACATGATATGA 721
DB 1583417 TTGAAAAAAGAGATATTTGAGCCACCAAACTTATTAATCAATGATATTCATCAACAATGA 1583358
QY 722 TTAAGAGAGAGATATGATGTCAGTGTATGATGTGACAGAGATGTTGGAGTTGTCATTCG 781
DB 1583357 TGGTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1583298
QY 782 TTGGTGTAAATTCCTGAAGATTTCTGAGTTATTCGAAGCAAGATCGAGGATTTCCGCTTG 841
DB 1583297 TTGGTGTAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1583238
QY 842 TTCTG 846
DB 1583237 CGATG 1583233
```

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RESULT 9
US-10-424-599-76259
; Sequence 76259, Application US/10424599
; Publication No. US20040031072A1
```

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; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yinhua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 76259
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(406)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_39876C.1
; US-10-424-599-76259

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Query Match
Best Local Similarity 14.9%; Score 145.4; DB 17; Length 406;
Matches 195; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 718 ATGATTAAGAGAGATATGATGTCAGTGTAGTGTGAGAGATGTTGGATTGTCA 777
Db 2 ATGANCAAAAGGAGGCGCATCTTTTGGTGTGACGGGCAAAAATGTTAGGGTTCCT 61
QY 778 TTGCTTGCTGATTTCTCTGAAGATTCGAGTATTTCGAGCAGATCGAGGTTCCG 837
Db 62 TTGCTCGGGTATTTCTCTGAGATGAGTATTAAGAACCCCAATAGAGTTTCCT 121
QY 838 CTGTTGTGATTAAGCCTCTAGCCTTGGCGGATTTGGCGTTGAGAGCGGCTTGAGA 897
Db 122 CTGTGTCTCAACAGCTCCCACTTTGGCCGGATTGGCGTTGCAACAAACCCGTTGAGG 181
QY 898 CTGTTGAGCAGATAGTATGAAAGGCTGTTATGTTGAGAGAGAACCTTAAGAAAGTGGC 957
Db 182 CTCGTGAGAGAGATAGATGACAGCGCGTGTGTGTGAGAAACAAAC--CAAACGTGGG 238
QY 958 TTCTTCTCTTCTTGGCGG 977
Db 239 TTTTCTCTCTTTTGTGGTGG 258

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RESULT 10
US-10-021-323-8529
; Sequence 8529, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jili
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 8529
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(545)
; OTHER INFORMATION: unsure at all n locations

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; OTHER INFORMATION: Clone ID: LIB3828-011-Q1-K6-D10
; US-10-021-323-8529

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Query Match
Best Local Similarity 14.7%; Score 143.8; DB 18; Length 545;
Matches 177; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 764 TGTGGGATTTGATCTTCTGTTAATTCCTGAAGATTGAGGTTATTCGAGCAGA 823
Db 1 TGTGGGATTTGATCTTCTGTTAATTCCTGAAGATTGAGGTTATTCGAGCAGA 60
QY 824 ATCGAGGTTTCCGCTTGTGTAATAGCCTTCCACCTTCCGAGATTGCGTTGAGC 883
Db 61 ACAGAGGATCCACTTGTGTAATAGCCTTCCACCTTCCGAGATTGCGTTGAGC 120
QY 884 AGCGGCTTGAAGACTGTTGAGCAAGATAGTAAAGCTGTTATGTTGAGAGAGAC 943
Db 121 AAGCGCTTGAAGGCTTGTGAGCAGATAGTAAAGGCTGTTATGTTGAGAGAGAC 180
QY 944 CTAGAAGAGTGGCTTCTCTCTTCTTCTTGGCGGC 978
Db 181 CCAA-AAGCTGGGTTTCTCATTTTGTGAGGC 214

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RESULT 11
US-10-767-701-26469
; Sequence 26469, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 26469
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(547)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: 30974845
; US-10-767-701-26469

```

```

Query Match
Best Local Similarity 13.5%; Score 132.4; DB 18; Length 547;
Matches 214; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 151 CCGAAGCTCCCGAGAAAGCGCGTATTCGTTATCACCCTCGGAAAGGCGGTGTT 210
Db 198 CCGAGCTCTGGGCGGACCCCGCGGTGTGTGTGCTTCCGGAAGGCGGCTC 257
QY 211 GGAAGAGCAGACACCGCAATGTGCTCTCTCTGCTGCTTACGTTTCTCAGTT 270
Db 258 GGAAGAGCAGACACCGCAATGTGCTCTCTCTGCTGCTTACGTTTCTCAGTT 317
QY 271 GTGCGATTGAGCGCGACCTTGTTGTCTCGTAACTCGATCTCTCTCCTAGAGTTAGAAAT 330
Db 318 GTGCGCGTGAAGCGCGACCGGCTTCGCAACTCTGACCTCTGCTGCGCTTCGAGAAC 377
QY 331 CGAGTCAATTACCTTGTGCTGAGTTAATAAGCAATTTGCTCTGATCAAGCTCTG 390
Db 378 CGCGTCACTCAACCGCGCGAGTACTCGCGGGAGCTGAGGCTCGACAGGCGCTC 437
QY 391 GTACGTATTAAGCTTGTGTGAATTTGCAATTTGTATGTATTAACCTTAGATCGAA 450
Db 438 GTCCGACACCGCGGCTTCACGAGACTTCACCTTGTGCTTCAAGCCCCCTCCAG 497

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QY 451 CTTCGATGGATTGGTGAAGATTGAATGCGTTGGATGCTT 500
 DB 498 CTGCGCTCGCGTTCGATCCAAAGACCTCACCCTGGTGGTGAACCGCT 547

RESULT 12

US-10-398-221-3303/c
 ; Sequence 3303: Application US/10398221
 ; Publication No. US20040018514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNST, Frederik
 ; APPLICANT: GLASER, Philippe
 ; TITLE OF INVENTION: *Listeria innocua*, genome and applications
 ; FILE REFERENCE: 344 702 - US
 ; CURRENT APPLICATION NUMBER: US/10/398,221
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 ; PRIOR FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: FR 00/12 697
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 4025
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3303
 ; LENGTH: 1987
 ; TYPE: DNA
 ; ORGANISM: *Listeria monocytogenes* 4b
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(end)
 ; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
 US-10-398-221-3303

Query Match 10.7%; Score 105; DB 17; Length 1987;
 Best Local Similarity 57.9%; Pred. No. 3.6e-22;
 Matches 186; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 526 GATTCATCATCATGATTTGCTCGAGAGATGATGCGGATTCATAACCGCATTTACT 585
 DB 1868 GATTTTATTTTATTTATTTATTTGCTCGAGAGATTTGATGATTTAAATGCGCTTGC 1809
 QY 586 CCGCGCAATGAAGACAGTTCTGTGAACAACCTCCGATATTAACAGCTTAAAGGATGCTGAT 645
 DB 1808 GGTGCGACGAACAAAGCAATTTGATTAACAACCCGAAATATACGCAATTTGATGAGAT 1749
 QY 646 AGCGTTACGGGTTTGTAAAGTCGATGATGATGATGATGATGATGATGATGATGATGAT 705
 DB 1748 AGAATTATCGGTTTACTGGAAGAAAGAAATATTGAGCCACCAAAATTTAATTAAACCGT 1689
 QY 706 GTGAGAACTGATATGATTTAAAGAGAGATATGATGATGATGATGATGATGATGATGATGAT 765
 DB 1688 ATTCGTAACAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1629
 QY 766 TTGGAGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 825
 DB 1628 TTATCAATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1569
 QY 826 CGAGGGTTTCGCGTTGCTG 846
 DB 1568 AGTGGGATCTGTTGCTATG 1548

RESULT 13

US-10-297-465A-1/c
 ; Sequence 1, Application US/10297465A
 ; Publication No. US20040142413A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Simpson, Andrew
 ; APPLICANT: Reinach, Fernando
 ; APPLICANT: Setudal, Joao
 ; APPLICANT: Mediane, Joao
 ; APPLICANT: Arruda, Paulo
 ; TITLE OF INVENTION: Isolated Genome of *Xylella fastidiosa* and Uses Thereof

FILE REFERENCE: FAPESP 202 US (10213376)
 ; CURRENT APPLICATION NUMBER: US/10/297,465A
 ; CURRENT FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01618
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: 60/209,906
 ; PRIOR FILING DATE: 2001-06-17
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 2731748
 ; TYPE: DNA
 ; ORGANISM: *Xylella fastidiosa*
 US-10-297-465A-1

Query Match 9.0%; Score 87.6; DB 18; Length 2731748;
 Best Local Similarity 50.6%; Pred. No. 1.1e-14;
 Matches 250; Conservative 0; Mismatches 229; Indels 15; Gaps 1;

QY 178 ATCGTGTATGACCTCCGAAAGCGGTTGGAAGACGACCAACCCCAATGTC 237
 DB 1272524 ATTATCGTATACATTTCCGCAAGGCGCGTTGGCAAAACGATACAGTGCACCTTG 1272465
 QY 238 GGTCTCTCTCTCGCTGTTACGTTTCTGAGTTGCGCATTGACGCGACCTTGCTTC 297
 DB 1272464 GCGTGGAGTTGGACAGACGCGGCAAAAAGTTGTAGTATGATTGACGTTGACCTT 1272405
 QY 298 CGTAACCTGATCTCTCTTAGGTTAGAGATCGATGATTAACCTTCCGCGAGCTT 357
 DB 1272404 CGCAACCTTGACCTCATATGAGGCTGCGCAACCCGCGTGTGATGACACTTGTCAACGTG 1272345
 QY 358 ATAAACGAGATTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
 DB 1272344 ATGATGCGGAAGCTATCAATCAAGCAAGCATCATCAAGCAAGGCTTCCAGACCTT 1272285
 QY 418 GATTGCTATGATATCTTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 DB 1272284 TATCTACTGCGCGCGCCCAACCCGCAAAAGCGCTTG-----ACT 1272240
 QY 478 TTGGAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
 DB 1272239 AAGGAGGGGTGAGAAAGTGTCTCAAGCTGCAAGAGAGGCTTGATGATGATGATGAT 1272180
 QY 538 ATCGATTGCTCGAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
 DB 1272179 TCGACTCTCCAGCTGATATGAGAGGCGCTCTCTGCGATGATGATGATGATGATGAT 1272120
 QY 598 GCAATCTGATTAACAATCCGATATTAACAGCGTTAAAGGATGATGATGATGATGATGATGAT 657
 DB 1272119 GCGTCTGCTGTGTAACCGGAGATATCTCGTGTGCGGATCAATGATGATGATGATGAT 1272060
 QY 658 TTGTTAAGATGCGA 671
 DB 1272059 CTGCTGACTCCAA 1272046

RESULT 14

US-10-335-977-3900
 ; Sequence 3900, Application US/10335977
 ; Publication No. US20040052799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DOUGLAS SMITH et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 ; RELATING TO HELICOBACTER PYLORI FOR
 ; DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 10031
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875

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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: CD-ROM ISO9660
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: Windows NT 4.0
/ SOFTWARE: UNIX
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/335,977
/ FILING DATE: 30-Dec-2002
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/993,002
/ FILING DATE: 17-Dec-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mandragouras, Amy E.
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: GTN-018
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 3900:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 807 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHEetical: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Helicobacter pylori
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (B) LOCATION 1...807
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3900:
US-10-335-977-3900

Query Match      8.3%; Score 81.4; DB 17; Length 807;
Best Local Similarity 49.1%; Pred. No. 7,8e-15;
Matches 337; Conservative 0; Mismatches 311; Indels 39; Gaps 3;

QY 179 TCGTCGTTATCACCTCGGAAAGCGGTGTGAAAGCGAACACCGCAATGTG 238
DB 11 TAGTTACTATCACTTAGGGAAGGGGGCGTGGCAAAAGCACACACGCGCTAATTAG 70
QY 239 GTCTCTCTCGCTCGTTACGTTTCTCAAGTTGTGCGCATTAACGCGCACTTGCTCC 298
DB 71 CGATTGCGTGGCTGAGAGCGGTAAAGTGTAGCGGTGATTGTCATAGGCTTA 130
QY 299 GTAACCTGATCTCCCTAGGGTTAGAGATCGATCAATTACACTTCCGTCGAGTTA 358
DB 131 GGAACCTGACATGATTTTATAGGCTTAGAAATCGCATGTTGTATGATGTGGATGTA 190
QY 359 TAAACGGAATGTGCTCTCGATCAAGCTCTGTACGTGTAAGCGGTGGTGAATTTG 418
DB 191 TGGAAAAAATTGCAACCTTTCACAGGCTTTGATCAGATTAAGAAAAAGATAAACTTT 250
QY 419 AATTGTATGTATATTAACCTAGATGCAAACTTCCATGGAATGGATTTGTGTAAAGCAT 478
DB 251 CTTTATTACGGGCTTCACAAAGTAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 295
QY 479 TGAATGCGCTGTGATGCGTTGAAATCTAGACCGGAAGTTACCGGATTTTATCATCA 538
DB 296 AGGAAAAATGACGATTTTATTAACACGCTTTTAAAGGCGGATTTT---GACTATATTTTGA 352
QY 539 TCGATTGTCGACAGAAATCGATGCGGATTCATTAACCGCATTAATCCGCGAATGAAG 598
DB 353 TTGACTTCACCGGCTGGGATGTAAGCGGTTTGTAGCATGCGATTTTGTATCGGACATGG 412
QY 599 CAGTTCTGGTAAACAACCTCCGATATATAACAGCTTAAGGATGCTGATAGGGTTA 658
DB 413 CGTTAGTGTGTAAAGCGGAGATGAGTTCCTTAAGGGATAGCGACAGAGTGAATGGCA 472
QY 659 TGTTAG-----AATCGATGGAATCAGAGATTAAGATTAAGATTAAGATTAAG 697

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DB 473 TTATGACGGAAGTCTAATCGGGCCAAAAGTGGGGAAGATGCATAGCATTTGATTA 532
QY 698 TGAACAGATGAGAACTGATATGATTAAGAGAGAGATTTGATGTCAGTTAGATGTC 757
DB 533 TCATGCTTAAACCTGAGTTAGTGGCAATGGGAGATGATGATTTCCATAGAAAGATGC 592
QY 758 AGGAGATGTTGGATTTGATTCATTTGTTGTGTTATTCCTGAAGATTCGTAGTTATTCGA 817
DB 593 TTAAATCTTTGTGCTTGCTTTAATTGGATTCATTCGTAGATCACCATATTATTTCAG 652
QY 818 GCAAGATGAGAGGTTTCCGCTTTC 844
DB 653 CCACCAATTAAGGCGAGCGGATTC 679

RESULT 15
US-10-672-787-13/c
/ Sequence 13, Application US/10672787
/ Publication No. US20040067554A1
/ GENERAL INFORMATION:
/ APPLICANT: LAGACE, Robert, R.
/ APPLICANT: PATTERSON, Chandra
/ APPLICANT: BERG, Kim, L.
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
/ FILE REFERENCE: ELITRA.025C1
/ CURRENT APPLICATION NUMBER: US/10/672,787
/ PRIOR FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: 09/596,002
/ PRIOR FILING DATE: 2000-06-16
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: PERL Program
/ SEQ ID NO 13
/ LENGTH: 31940
/ TYPE: DNA
/ ORGANISM: Moraxella catarrhalis
US-10-672-787-13

Query Match      7.5%; Score 73; DB 17; Length 31940;
Best Local Similarity 54.2%; Pred. No. 3,3e-11;
Matches 148; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 178 ATCGTCGTTATCACCTCGGAAAGCGGTGTGAAAGCGAACACCGCAATGTG 237
DB 273 ATCGTTGATGTAAGTCAAGTTAAGGCGGTGCGCAAAACACACAGTGCATCAATT 214
QY 238 GGTCTCTCTCGCTCGTTACGTTTCTCAAGTTGTGCGCATTAACGCGCACTTGCTC 297
DB 213 GTGCAAGGCTTGCTAGCGTGGCTTTAAACAGTATCATTAATGATGTCGTTG 154
QY 298 CGTAACCTGATCTCCCTAGGGTTAGAGATCGAGTCAATTACACTTCCGTCGAGTT 357
DB 153 CGTATTTATGATCTAATTATGAGGTGTGAAATCGATGCTCATATCACTTTGTAGATG 94
QY 358 ATAAACGGAATGTGCTCTCGATCAAGCTCTGTACGTGTAAGCGGTGGTGAATTTT 417
DB 93 ATCAGGTGTAATCCAAAGCTTGCTCAAGCTTATGTCAAAAGACAAATTTGAAAAATCTA 34
QY 418 GAATTGTATGTATATTAACCTAGATGAAA 450
DB 33 TACATTTTGGCTGATCGCAAAACGCGAGACAAA 1

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Search completed: March 10, 2005, 23:46:33
Job time : 618 secs